GVHGQHGGHVTHADIGGATVMEIDPSQIKHEPGMIITPEIVNMMSSGHM 653	Db 605 C
LLVANSGIMNEGLLNLLSASQENSNGNASLLLQQQQHQQHQQHHQQHQQQQQQOVVAAYR- 552	Oh 573 -
QH	Db 563 -
RGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKG 493	Эγ 434 Я
НОДАНООНО 562	กb 544 H
HDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGSDLGEDVD 433	Эу 374 Н
VKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKH 373	рь 502 -
QQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSS	2y 263 C
GVTSTGQAIVTQIVVARDGKDTKNMTSLGMGMNGGLLGVPMGFLDFT	396
AATPANSLELYKLITQRAAKMTSMD-SMAAQLAQESL-LADENLINSLASQQQQQQ 262	م 209 کر
HTHGHGHSHDHSHDHEHEHKPNKICKTEHSVASPASNSSSASNNAAGVS 39	346
STSNSHIHOHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPA 208	Эу 157 -
IDWRPSAKCNFCVNGRLITVNAQGKLVAESAATATSS 156	Oy 120 I
ASGSSGSLAGGQQASQTPSGLQPTPRKSRLKRSKSPDLSSGGGAGSSGGSSSGSTQQ	Db 226 S
DSENNQTSHDSSRTPTP	Эу 90 Е
EPSQYNHSSKEISOSNPNHCKTENHRLEQOHNGSQLLEE 89	2y 51 E Db 166 E
1 4.4%; Score 263; DB 2; Length 1085; Similarity 17.9%; Pred. No. 1.2e-05; 6; Conservative 135; Mismatches 398; Indels 458; Gaps 44;	Query Match Best Local Si Matches 216;
ak; psq : II /3 required for establishing polarity of the developing egg chamber BRcore-Z protein; POZ domain homology n: POZ domain homology <poz></poz>	A;Gene: pipsqueak; A;Map position: II A;Introns: 427/3 C;Function: requ Tuperfamily: BRco :-123/Domain: PO
1-355,'E', 357-1005,'H',1007-1020,'Q',1021-1061,'ERS' <hor> rences: EMBL:U48358; NID:g1203906; PIDN:AAC47153.1; PID:g1203907 al source: tissue type ovarian</hor>	A;Residues: 1-355,'E', A;Cross-references: EM A;Experimental source:
JI: 19961 STORE MRNA STORE MRNA	A;Status: prelim
122, 1859-1871, 1996 122, 1859-1871, 1996 Drosophila pipsqueak gene encodes a nuclear BTB-domain-containing protein r number: Z22972; MUID:96232300; PMID:8674425	Development 122, 18: A;Title: The Drosopl A;Reference number:
2: DNA 2',428-1085 <we2> CCES: EMBL:X90986; NID:G1149498; PIDN:CAA62475.1; PID:G1149501</we2>	Molecule t Residues: Cross-refe
eferences: EMBL:X90986; NID:g1149498; PIDN:CAA62474.1; PID:g1149500 preliminary	A;Cross-reference A;Accession: S661 A;Status: prelimi

	KANKOKR 1085	1079	ઠ
	GNGRSSR 1086	1080	Ş
CRK 1078	QQSPHPGHHPQHMQQDVVTSSSQVVHSQQQQQLQQIYQHHGTPVTASGSSAVSGGTSKRK 1078	1019	В
)TN 1079		1040	γ
8101 000	LQQQFPYSPSPHPPTPQHHSTPQHHSSAQQGPPTPQHMQQYVVHMQQQQQQQQ 1018	966	В
NDS 1039		984	Ş
296 WH	SLYGREKRGKYDVVANT	920	В
HA 983	AQDMVENVYDGIIRKTLQASEGNGSAAGNGSNGSNGHGHGHGHGHA 983	936	δ
919 SY		873	B
1KS 935	ATFNGLKLPLFEAGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKS 935	876	Ş
'GR 872	LAAPENAAPTTWTPEDLERALEAIRAGNTSVQKASAEFGIPTGTLY	825	В
AA 875	LTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAA 875	829	δ
824	SWNEDALQNALEALRSGQISANKASKAFGIPSSTL-YKIARREGIR	780	дb
VG 828	NYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVG 828	. 769	γ,
TK 779	SLTKASAIYGIPSTTLWQRAHRMGIETPKKEGGTK 779	745	ф
YR 768	SISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQQLSAQEALGKGTRPKRGKYR 768	709	8
744	GMSGGAGSGSGEKGQFNGPKAWTQDDMNSALDALKNQNM	706	В
KP 708	GYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKP 708	649	δ
igg 705	DMYNSDTSEDSMMIANGSPHDQKEPHYTNLDQQHGLGGSVCGPGPGGAGG	654	Вb
- QG 648	605 HPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQG 648	605	8

Search completed: October 29, 2003, 12:31:30 Job time : 64 secs

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Maximum Match 100%
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.bAT: *
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query Match	Query Match Length DB	BD	ID		Description
щ	6030	100.0	1165	23	AAE24372	1	Fruit fly E93 prog
2	5882	97.5	1140	22	ABB71145	•	Drosophila melanog
ω	4839	80.2	1221	23	AAE24373		Fruit fly E93 prog
4.	314.5	5.2	1937	22	ABB58985		Drosophila melanog
v	314.5	5 . 2	2151	22	ABB60086		Drosophila melanoq
σ	311.5	5.2	2112	22	ABB60403		Drosophila melanog
7	299.5	5.0	2175	22	ABB65698		Drosophila melanog
8	296.5	4.9	1161	22	ABB70667		Drosophila melanog
9	294	4.9	2441	22	ABB62231		Drosophila melanog

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ABB51650 ABB58077 AAAO22566 ABB58077 AAAO22566 ABB58070 AAB58382 ABB685702 ABB59862 ABB59862 ABB59862 ABB661547 ABB6622 ABB66237 ABB662637 ABB602676 ABB760377 ABB67676 ABB760377 ABB677676 ABB760377 ABB677676 ABB760377 ABB677676 ABB760377 ABB677676 ABB760377 ABB677676 ABB760377 ABB677676 ABB71576 ABB68776 AB6	ABB61959 ABB60040 ABB61328 ABB66223 ABB65499 ABB60091 ABB60091
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ALIGNMENTS

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04-OCT-2002 (first entry)
                                                                      AAE24372 standard; Protein; 1165
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Fruit fly E93 programmed cell death modulating protein #1.

RESULT 1
AAE2437
ID AAE25
ID AAE25
XX AAE2
AC AAE2
XX AAE2
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DE Frui
XX Fruit fly; programmed cell death modulating protein; adenocarcinoma; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; Alzheimer's disease; retinitis pigmentosa; Parkinson's disease; myelodysplastic syndrome; cerebellar degeneration; applastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytostatic; melanoma; neuroprotective; myeloma; nootropic; vasotropic; immunostimulant; cerebroprotective; cardiant; cancer; E93 protein.

Drosophila melanogaster.

WO200234882-A2

02-MAY-2002.

29-OCT-2001; 2001WO-US48053.

27-OCT-2000; 2000US-243865P.

(UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

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The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the compounds are useful to screen potential cellular apptosis inhibiting compounds to determine their use as therapeutic agents for treatment of compounds to determine their use as therapeutic agents for treatment of compounds to determine their use as therapeutic agents for treatment of compounds to determine their use as sociated with decrease in compounds to retain or preventing disorders associated with decrease in compounds or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, compounds of the activity of the sequences of the compounds of the compounds of the sequences of the compounds of the sequences of the compound of the sequences of the compound of the sequences of the compound of the sequences of the pigmentosa, parkinson's disease (e.g., Alzheiner's disease, retinitis compound of the sequences (e.g., Alzheiner's disease, retinitis compound of the compound of the sequences (e.g., Alzheiner's disease, retinitis compound of the compound of the sequences (e.g., Alzheiner's disease, retinitis compound of the compound of the sequences (e.g., Alzheiner's disease, retinitis compound of the sequences (e.g., Al
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                                                                                                                                                      SEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPK
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standard; Protein; 1221 ጅ

entry)

cell death modulating protein

Fruit fly; programmed cell death modulating protein; adenocarcinoma; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS neurodegenerative disease; Alzheimer's disease; retrinitis pigmentosa; Parkinson's disease; myelodysplastic syndrome; cerebellar degeneration; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytostatic; melanoma; neuroprotective; myeloma; nootropic; vasotropic; immunostimulant; cerebroprotective; E93 protein AIDS;

BIOTECHNOLOGY INST

Novel programmed cell death modulating proteins, useful for treating preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction õ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel programmed cell death modulating proteins and polymucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapputic agents for treatment of diseases associated with increased programmed cell death. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for
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SSSIQKWMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTD
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36; Mismatches
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                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                            (ABB57737-ABB72072)
                                                                                                                                                                  Disclosure; SEQ ID
                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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                                                                NPYSLGSSGLGSAYDQ--LAQQYNLLNGATSSASNTSSTQSKSHQSQSKSSQSRNTTASA
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                 Disclosure; SEQ ID NO 8001; 21pp + Sequence Listing; English
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                          ENVYDGIIRKTLQASEGN-GSAAGNGSNGSNGNGHGHGHGHGHALLDQLLVKKTPLPFTN
                                                                                  PLFEAGPOALSFOPNMFWPQTNATNAYGLDFNR---ITEAMRNPQASNHHGLMKSAQDMV
                                                                                                                                         PDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAAATPNGLKL
                                                                                                                                                                       PDGECQDTETYLADKKDCARFYRCVENGSGGFNKVPFDCSPGTVWD-------
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26 YQDKLTCSHLNIEEQQPIAIAGSEDEPSQYNHSSKEISQSNPN------HCKTENHRL

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Mismatches

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Best Local Similarity Matches 256; Conserv
                          Query Match
                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The inventuateful in developmental biology and in elucidating cell signalling cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                       Sequence
                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23886; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and
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N-PSDB; ABL09801.
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11-JUL-2000;
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  LPFTNHRNNDYAA----
                                                   LIARTPRETAFPSFLFSPSLFGGAAGMPGAASNA-
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NGSSGSSHGSPHKRASSHSLEEEHLQQHREQQLQQQQQ
                                          PGH------HTTSILHEKLAQIKAEQVDQADQ 1164
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Local Similarity 19.8%; Pred. No. 8.8e-11;
les 246; Conservative 145; Mismatches 437
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   186 SNNNSSGNR-----ARHIAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSM--
                                                                                                                                                                                 SKLQSSESASNINS--STATNTSSANTTRKEVAKPASQTASAT---TLNPAKRTEVDGWK 141:
                                                           EVVRKSSÄQQTTAVGASGAPLPVTÄTSSATSVQHHPHHHLANSSSNSSSSLTTSTTTAAS
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                                                                                                                                                         HGHGHGHALLDQLLVKKTPLPFTNHRNNDYAATCSSASGESV 1017
                                                                                                                                                                                            QPPGT---GARQPGGAAAQRWYGGTLEYPSYTGRDMLHLENGAGGMAGMGSPSAMSPNHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The inventues full in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7373-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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11-JUL-2000;
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KPLSAE - - -
                               I PLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLNLLSASQEN
                                                                                                                                        SILDWAGYIDQGKQLSILHSLLSESLAKLPEARQHELDPLQHILDEISRAKEHGMGTAL-
                                                                                                                                                                         SILD-----NRLFKMKHH------DQEQDHDGDELEDSNDDAEAEVDSNASTPVY
                                                                                                                                                                                                              ----AKTLQTLANFT----RFQGKENFMEFLNDFLEQEAARMQQFLEIISTRPEHPAPD 566
                                                                                                                                                                                                                                               SISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANK-----LDARKSASQHHEQR
                                                                                                                                                                                                                                                                                 QLGRODMADNL-----ISASIFLRFLCPAILSPSLFNITSELPSARATRNLTLV----
                                                                                                                                                                                                                                                                                                                    QQQQQIASAVTPTTSEVSA-----AAISPALKDTPS--PSVDAPLDLSSKPSPNS
                                                                     PGGYLPATSSTHSIASENQENRNPGSSGSHAGSNSEQLLPQQSQ-----LAQPQHAIVS
                                                                                                    PAEFARAQLRKLSHLSEH----
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Pred. No. 4.9e-11;
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                  Drosophila melanogaster
                                                    pharmaceutical.
                                                                 Drosophila; developmental biology; cell signalling;
                                                                                                     Drosophila melanogaster polypeptide
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                                                                                                                                                                                                           ABB60040 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                     GQTNGNGRS------SRMTSRDDSETDASSFKSGENGGQQNHKMMDLNG
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Matches 205; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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11-JUL-2000;
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AQLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLML
                              QQQQQQQLLTLQQQRERELQQQQQQQQQHQRELHPPTTHILPASAVYSIESSEVLPTAAPR
                                                                 SASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAE-VDSNASTPVYPAEFAR
                                                                                                    PQPAP----PPPPKPKIVNTFTEIPGTTGVGSSYAKEQQQQQQLLALQ-
                                                                                                                                    SVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARK 352
                                                                                                                                                                                                        Q-----FSLLADFNLINSLASQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSP
                                                                                                                                                                                                                                          KCATLRHVGRYGGSLKGVSAVNATPSPAAAPAVHSPNL----RSAKTPSIATVSKDYC
                                                                                                                                                                                                                                                                           ----ARH-----IAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLA
                                                                                                                                                                                                                                                                                                               GICRSTGNGLDGDMVDDRDPRDVTNNSFNRFDPKYISIGPKAVRGQNNNLNIMSVAGGAN
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                                                                                                                                                                       SNTAQQQQQNLQLQQHQQQSNLINQNQSQSTLKNIFASATLPRSTGSSIRSVLSVQTSNA
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; Pred. No. 1.2e-10;
85; Mismatches 351;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                               Disclosure; SEQ ID NO 10776; 21pp + Sequence Listing; English
                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                              Venter
                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                    PPPLRAPVQQQRNNLSVDQPNSMTG-----NNGIYKKNVFGPNQ-------
                                                                                                                                                                                                                                                                                                                     IGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSL 775
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    PSIRPSELVRGNHNRTMSTISANKKAKLL-NAGSTNGSSIAASSDDS-QSRYGGSVH---
                                                                                            TN-----ANGTGGAA--
                                                                                                                                          ANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAATPNGLKLPLFEAGPQA
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Pred. No. 1.6
                                                                                                                                                                                                                                                                               -NLKRVSSAPPMQNL----AVVNGPPP
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                                                                                               PPPVPAPNPVATEAVDSDSGLEV----VEE
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Matches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 25461; 21pp + Sequence Listing; English
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genes from Drosophila
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genes from Drosophila and
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                                                   AKSDDDLDEVDRITNCSVLLQLSNGNG----GDISKVTGSSKTRAECKRAKNSKNQA---
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                                                                                                                                                            GAPASIPLDANVLLHTLMLAAG-----
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Pred. No. 2.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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1 US-08-185-432-19 4 US-08-189-232-4 5 US-08-10-517-2 2 US-08-853-310-2 2 US-08-853-310-2 4 US-09-125-635-4 1 US-09-264-604-2 2 US-08-642-846-2 4 US-09-264-604-2 4 US-09-264-604-2 5 US-08-061-376-5 5 US-08-061-376-5 6 US-08-147-236-5 7 US-09-147-236-5 7 US-09-147-236-5 8 US-08-891-640-2 3 US-08-891-640-2 3 US-08-891-640-2 3 US-08-891-640-2 3 US-08-195-152-2 4 US-09-256-877-179	1776	760	1257	1464	1326	1326	842	3969	951	1664	1664	1664	1420	903	1581	2703	2703	
US-08-185-432-19 US-08-899-232-4 US-09-110-517-2 US-08-853-310-2 US-09-155-635-4 US-09-155-635-8 US-09-164-604-2 US-09-165-635-8 US-09-165-635-8 US-09-165-635-8 US-09-164-60-2 US-09-164-60-2 US-09-164-60-2 US-09-164-5 US-09-164-5 US-09-1640-2 US-08-91-640-2 US-08-91-640-2 US-08-955-152-2 US-09-556-877-179	4.	_	w	w	4.	4	ហ	w	4	4	N	_	4	N	w	4	۲	
	US-09-556-877-179	US-08-195-152-2	US-09-220-641-3	US-08-891-640-2	US-09-522-474-5	US-09-147-236-5	PCT-US96-02331-15	US-08-061-376-5	US-09-125-635-8	US-09-264-604-2	US-08-642~846-2	US-09-599-652-2	US-09-125-635-4	US-08-853-310-2	US-09-110-517-2	US-08-899-232-4	US-08-185-432-19	
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19, 22, 22, 24, 44, 44, 44, 44, 44, 44, 44	Sequence 179, App	Appli	Appli	Appli	Appli	Appli	Appl	Appli	Appl									

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4463
LENGTH: 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463
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GEMERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND ANTITLE OF INVENTION: EDIDERMIDIS FOR DIFILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 EPSQYNHSSKEISQS---NPNHCKTENHRLEQQHNGSQLLEE-----EDSENNQTSHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                              SSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAGGKLVAESAATATSSSTSN 160
                                                                                                                                              SEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEE
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DSTSESTSLSESLSTSVSDSTSASTSESA---
                                                       D-----LSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELED
                                                                                                                                                                                                                       VSDSTSTSTSDSASMSASESES------NSKSTSLSESTSTSLSGSTSAST
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                                                                                                           SDSASTSTSESESDSTSTSL----SESTSTSLSGSTS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%; Score 252; DB 4; I ilarity 17.1%; Pred. No. 2.5e-09; Conservative 208; Mismatches 539;
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  --STSTSESESNSASTSLSG
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GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-99
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASLSEQ for Windows Version 4.0
SOFTWARE: FASLSEQ for Windows Version 4.0
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US-09-914-259-37
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                                                                                                                                                                                                                                                                             Sequence 37, Application US/09914259 Patent No. 6495336
       LENGTH: 1507
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                                          1160 LQQPAIKLLNGASIAPVNTK-----ATIRLVE------SKPPTTTQSR 1196
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VKERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGP----
                                                                                      SAQEAL----GKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEYK 806
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RESULT 3
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Patent No. 6040140
GENERAL INFORMATION:
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APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute |
TITLE OF INVENTION: Resulting from Chromosome Abnormalitic
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/32/,JEFILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US 08/320,559
             FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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APPLICATION NUMBER: 1
FILING DATE: 09-DEC-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 22-APR-
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APPLICATION NUMBER: US,
FILING DATE: 07-MAR-199
CLASSIFICATION: 435
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                                                                                     FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                FILING DATE:
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                                                                   APPLICATION NUMBER:
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MAKVNLV-PQQQQHGNKRHLNSATGAGNPVESKRLKSGTLCLDVQSPQLLQQLIGKDPAQ
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                                                                                                                                                                                                                                                                     NUMBER: PCT/US92/10930
09-DEC-1992
                                                                                                                                                                11-OCT-1994
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27-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for Detection and Treatment of Acute Leukemias Resulting from Chromosome Abnormalities in the All-1 Region
                                                                                                                        US 08/062,443
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                            PALFDQTAS-----
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                                                                                   ALQKENQRLQEQILSLTAKKERLQILNVQLSVPFPALPAALPAANGPVPGPYGLPPQAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116;
                                                                                                                                                            --APCGGGQLDPAAPGTTNMEQLLEKQGDGEAGVNIVEMLKALH
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             STSKSPPG-----KSSLGLDNSLSTSSEDPHSGCPSRSSSSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 231; DB 3; I
Pred. No. 3.3e-08;
L6; Mismatches 373;
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                                                                                                                                                                                                                                      -----CRGTSPQESLSSMSP-----
                                                                                                                                                                                                                                                                                                            ----AGSTFSLPSTHIFGTPMGAVNPLLSQ 641
                                                                                                                        -----KSETPETNS----SLDPNDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMDSMAAQLAQFSLLADF 248
                                                                                                                                                                                                                                  ----ISSL
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Query Match 3.8%; Score 231; DB 5; Length 1093; Best Local Similarity 19.9%; Pred. No. 3.3e-08; Matches 206; Conservative 116; Mismatches 373; Indels 342; Gaps 40;		; TOPOLOGY: linear MOLECULE TYPE: protein	2 3	; INFORMATION FOR SEQ ID NO: 55; ; SEQUENCE CHARACTERISTICS: : INFORMATION SERVICES:	; TELEPHONE: (215) 568-3100 ; TELEPAX: (215) 568-3439	꽂낊	; NAME: DeLuca Esq., Mark ; REGISTRATION NUMBER: 33,229	CLASSIFICATION: PHYDRIPS / ACENT INFORMATION.	; APPLICATION NUMBER: PCT/US94/04496 ; FILING DATE:	SOFTWARE: Patentin Release #1.0, Version #1.25	; COMPUTER: ITELY CLOPY CLOS. ; COMPUTER: DC compatible ; ODERATING SYSTEM: PC-DOS/MS-DOS	ER READABL	COUNTRY: USA	; CITY: Philadelphia ; STATE: Pennsylvania	3: Norris One Liberty Place, 46th floor	; CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &	TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 NUMBER OF SEQUENCES: 86	li Therapeutics and Methods Therapeutics and Methods	INFORMATION: CANT: Croce, Ca			Db 1059 AOTNEFFISISGAEGSGG 1075	р с о н		956 SPQLTFEHQTVVXQMLQQIQQKRELQKLQMAGGSQLFMASLLAGSSTFLLSAGTFG	793 GSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGPHG	Db 931 SLTEQQRHLLQQQEQQLQQLQLLA 955	Qy 733 QQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRA 792	876 -GAMPMAEGLLGGLAGSGGLPLNGLLGGLNGAAAPNP	687 NGNVSDCSSNNGGSSST.GVKKPSTSVSTTGGTDTSSEGGSSTTTG	QY 634 PHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLR 686
₽ %	? 문	y V	g &	?	. Q	Дb	Q ·	. Db	Qy	Дb	Qy	DЬ	ν	Дb	Qy	Db	Ş	Db ?	Q	B 8	Дb	Qy	מם	νQ	Дb	γQ	מ א) b	. Q	В	ΟΥ
1059 AQTNPFLSLSGAEGSGG 1075	1012 LLETASAPPLLPAGALVAPSLGNNTSLMAAAAAAAAAAAAAAGGPPVLT 1058	LFEAGPQALS	956 SPQLTPEHQTVVYQMIQQIQQKRELQRLQMAGGSQLPMASILAGSSTELLSAGTEG 1011		RPKRGKYRNYDRDSLVĘAVKAVQRGEMSVHRA Į	876 -GAMPMAEGLIGGLAGSGGIPINGLIGGLNGAAAPNPASISQAGGAPTIQIPGCIN 930	687 NGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLS 732	830 FHSTPPPLPLLQQSPATLPLALPGAPAPLPPQPQNGLGRAPGAAGL- 875	634 PHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLR 686	788 SDSLSTSKSPPGKSSLGLDNSLSTSSEDPHSGCPSRSSSSLS 829	574 EDPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSNSHRNGSNRS 633	728 ALQKENQRLQEQILSLTAKKERLQILNVQLSVPFPALPAALPAANGPVPGPYGLPPQAGS 787	535 HQQHHQQQQQQHVAAYRHRLPKSETPETNSSLDPNDAS 573	677 PALFDQTASAPCGGGQLDPAAPGTTNMEQLLEKQGDGEAGVNIVEMLKALH 727	479 PKL-DETQTVGDFIKGLLVANSGGIMNEGLLNLLSASQENSNGNASLLLQQQQHQQH 534	642 AEŚSHTEPDĹEDCSFŔĆRGTŚPQESLSSMSPÍSSL 676	419 HLGEHNGSDLGEDVDRGSPKNGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAM 478	SISTTOVESLAGSTESLESTHIEGTEMGAVNELLSO	359 EQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLS 418	305 SPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHH 358	511ASPFSGGSLVSSGLGGLSSRTFGFS-GSLPSLSLESPLLGAGIYTSNK 557	249 NLINSLASQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKP 304	458 TPETGLKEKKHKASKRSRHGPGRPKGSRNKEGTGGPAAPSLPSAQLAGFTATA 510	211 TPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADF 248	404 GPIMRFSTTTSSSGRARAPSPGDYKSPHVTGSGASAGTHKRMPALSATPVPADE 457	RHIAAASARATPAAA	355 FSAFPKLEQPEEDKYSKPTAPAPSAPPSPSAPEPPKADLFEQKVVFSGF 403	ESKGKKSSSHSLSHKGKK	-PNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTPGATST	237 GQKKSRKDKERLKQKHKKRPESPPSILTPPVVPTADKVSSSASSSSHHEASTQETSESSR 296	19 GRRQWKHYQDKLTCSHLNIEEQQPIAIAGSEDEPSQYNHSSKEISQSN- 66

218 LYKLLTQRAAKWTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQQIAS	QY 165 QHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLE 217	Qy 108 GATSTDSPPPEDIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH 164 :	QY 49 EDEPSQYNHS-SKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTP 107	Qy 2 HISSYEISLERVAEECMGRRQWKHYQDKLTCSHLNIEEQQPIAIAGS 48	Query Match 3.8%; Score 229.5; DB 1; Length 2843; Best Local Similarity 19.3%; Pred. No. 1.6e-07; Matches 266; Conservative 179; Mismatches 510; Indels 421; Gaps 63;	AMINO ACID Y: linear TYPE: protei 2	; TELEFAX: 202-508-9299 ; INFORMATION FOR SEQ ID NO: 2: ; SEQUIENCE CHARACTERISTICS: ; LENGTH: 2843 amino acids	; REGISTRATION NUMBER: 32,141 ; REFERENCE/DOCKET NUMBER: 1107.035574 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 202-508-9100	; FILING DATE: 19920109 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: Kagan, Sarah A.	OPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/741,940	ZIP: 20001-4598 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC Compatible	01 G Street, NW ington	INVENTION: F SEQUENCES: NDENCE ADDRES SEE: Banner,	MARKHAM, NAKAMURA, THLIVERIS NVENTION:	GRODEN, HEDGE, P. JOSLYN, KINZLER,	ICAN I	RESULT 5 US-07-741-940-2 ; Sequence 2, Application US/07741940 ; Patent No. 535775
Qy 1102 SGENGGQQNHKWMDLNGGSSSSSHIKCESEAATGHHSPGHHTTS 1145	QY 1048SASHINNNNSDLAHNKNKSGGGGGGGGNGQTMGNGKSSRMTSRDDSETDASSFK 1101	2080 LKDIQ	: : : : :	CV 996 PFTNHRN	µ	QY 828 GLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAATPNGLKLPLFE 887	Qy 779 VKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLV 827	Qy 720 DTSRFGASPNILSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKY-RNYDRDSLVEA 778	Qy 666 KMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719	QY 625 SHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSSIQ 665	Qy 579 K-IPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSN 624	Qy 547 HVAAYRHRLPKSETPETINSSLDPNDASEDPIL 578	Qy 487 VGDPIKGLLVANSGGIMNEGLLNLLSASQENSNGNASLLLQQQOHQQHHQQHQQOQQQQ 546 : :	Qy 429 GEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQT 486	Qy 377 EQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGSDL 428	Qy 329 RAYSEEDLSRALQDVVANKLDARKSASQHHEQRS-ILDNRLFKMKHHDQ 376 :: : : : : : :	QY 269 AVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGR 328

Qy 218 LYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIAS 268 	Qy 165 QHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLE 217	Qy 108 GATSTPSPPPBPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH 164	CY 49 EDEPSQYNHS-SKEISQSNENHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTP 107	2 HISSYEISLERVABECMGRRQWKHYQDKLTCSHLNIEEQQPIAIAGS	Query Match 3.8%; Score 229.5; DB 1; Length 2843; Best Local Similarity 19.3%; Pred. No. 1.6e-07; Matches 266; Conservative 179; Mismatches 510; Indels 421; Gaps 63;	; TOPOLOGY Inear ; MOLECULE TYPE: protein US-08-289-548A-2	RISTICS:	INFORMATION FOR SEO ID NO: 2:	TRATION ENCE/DC MUNICAT	; FILING DATE: 12-AUG-1994 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: KAGAN SAYAh A	; OPERATING SYSTEM: PC_DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/289,548A	; ZIP: 20001-4598 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER; IBM PC compatible	001 G Street, NW hington C. USA	VVENTION: GENE IN COLORE SEQUENCES: 102 ENCE ADDRESS: 3: Banner & Allegretti,	: MARKHAM, : NAKAMURA, : THLIVERIS	: GRODEN, : HEDGE, P : JOSLYN, : KINZLER,	LICAN	RESULT 6 US-08-289-548A-2 ; Sequence 2, Application US/08289548A ; Patent No. 5648212
Qy 1102 SGENGGQQNHKMMDLNGGSSSSSHIKCESEAATGHHSPGHHTTS 1145 :	Cy 1048SASH.NNNNSDLAHNKNKSGGGGGGGNGQTNGNGKSSKWTSKDDSETDASSFK 1101	2080 LKDIQ	Db 2020 CFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLD 2079	L	Qy 888 AGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRN-PQASNHHGLMKSAQD 938	Db 1877EKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920	1834VRĠSFAFDŚPHHYTPIEĠTPYCFSRNDSLŚSLDFDDDDVDLSR	Qy 779 VKAVQRGEMSVHRAGSYYGVPHSTLEYKVKBRHLMRPRKREPKPQPDLV 827	Qy 720 DTSRFGASPNILSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKY-RNYDRDSLVEA 778	Qy 666 KMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719	Qy 625 SHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQ 665	Qy 579 K-IPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSN 624	Qy 547 HVAAYRHRLPKSETPETNSSLDPNDASEDPIL 578	Qy 487 VGDFIKGLLVANSGGIMNEGLLNLLSASQENSNGNASLLLQQQQHQQHHQQHHQQHQQQQQQ 546 : : : : : : : : :	Qy 429 GEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQT 486	OY 377 EQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGSDL 428 .	Qy 329 RAYSEEDLSRALQDVVANKLDARKSASQHHEQRS-ILDNRLFKMKHHDQ 376	Qy 269 AVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGR 328

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Patent No. 5691454
                                                                                                                                                                                                                                                                                                                                                   Matches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
-08-452-654-2
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FILING DATE: 25-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Banner, Birch, McKie & Beckett STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                  1196 SFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSIN 1259
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                                                        QHDSDSNSSASLPHHISSSSSSSNNNSSGNRAR----HIAAASARA---TPAAATPANSLE 217
                                                                                                                                         GA---TSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH 164
                                                                                                                                                                                 ETNRVGSNHGINONVSOS---LCQEDDYEDDKPTNYSERYSEEB-----QHEEEERPTN 1161
                                                                                                                                                                                                                     EDEPSQYNHS-SKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTP
                                                                                                                                                                                                                                                                                                   HISSYEISLERVAEECMGRRQ---WKHYQDKLTCSHLNIE----EQQPIA-----IAGS
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
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19.3%; Pred. No. 1.6e-07;
ative 179; Mismatches 510;
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                                                                                                                                                                                                                                                                                                                                             Indels 421;
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Qy 269 AVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGR 328	Qy 218 LYKLLTQRAAKMTSNDSNAAQLAQFSLLADFNLINSLASQQQQQQQQQIAS 268	Qy 165 QHDSDSNSSASLPHHISSSSSSNNNSSGNRAR	Qy 108 GATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH 164 :	Qy 49 EDEPSQYNHS-SKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTP 107	Qy 2 HISSYEISLERVABECMGRRQWKHYQDKLTCSHLNIEEQQPIAIAGS 48	Query Match 3.8%; Score 229.5; DB 2; Length 2843; Best Local Similarity 19.3%; Pred. No. 1.6e-07; Matches 266; Conservative 179; Mismatches 510; Indels 421; Gaps 63;	amino acid Y: linear TYPE: protei	202 508 91 R SEQ ID N RACTERISTI 843 amino	TRATI	> N Z	SYSTEM: Patentl LICATION ON NUMBER	. KEO	; STREET: 1001 G STREET, N.W. ; CITY: WASHINGTON ; STATE: DC ; COUNTRY: US	OF INVENTIONS IN THE APC OF SEQUENCES: 4 PONDENCE ADDRESS: ESSEE: BANNER & WITCOFF, LTD.	: KINZLER, : HILL, DAV : JOHNSON, INVENTION:	Sequence 2, App Patent No. 5910 GENERAL INFORM APPLICANT:	RESULT 8 US-08-370-235A-2	Db 2186 KGIKGGKKVYKSL-ITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSS 2240
RESULT 9 US-08-449-731-2	Db 2186 KGIKGGKKVYKSL-ITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSS 2240	2140 SGISLG	WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLK KNKSGGGGGGGGGGOTNGNGRSSRMTSRDDSETDASSFK	1027 YADIKBEBISADS	1975 IDQENNNKENEDIKET-EPPDSQGEPSKPQ	–	Qy 828 GLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAATPNGLKLPLFE 887	Qy 779 VKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLV 827	Qy 720 DTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQBALGKGTRPKRGKY-RNYDRDSLVEA 778	Qy 666 KMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719	Qy 625 SHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQ 665	Qy 579 K-IPSEKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSN 624 :	Qy 547 HVAAYRHRLPKSETPETNSSLDPNDASEDPIL 578	Db 1512 DEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEK 1555	429 GEDUDRGSPKWGRHPACGNASANQGAPASIFIDANVLLH-TLMLAAGIGAMPKLDETQT		Db 1359 KSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQ 1406	1316 AEDP-VSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEF

Query Match 3.8%; Score 229.5; DB 4; Length 2843; Best Local Similarity 19.3%; Pred. No. 1.6e-07; Matches 266; Conservative 179; Mismatches 510; Indels 421; Gaps 63; Qy 2 HISSYEISLERVAEECMGRRQWKHYQDKLTCSHLNIEEQQPIAIAGS 48	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/449,731 FILING DATE: 25-May-1995 CLASSIFICATION: <unknown> PRIOR APPLICATION: <unknown> PRIOR APPLICATION NUMBER: 08/289,548 FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION: NAME: KASGAN, Sarah A. REGISTRATION NUMBER: 32,141 REFERENCE/DOCKET NUMBER: 1107.46943 TELEPONGE: 202-508-9100 TELEPHONE: 202-508-9299 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2843 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-08-449-731-2</unknown></unknown>	Sequence 2, Application US/08449731 Patent No. 6413727 GENERAL INFORMATION: ALBERTSEN, HANS APPLICANT: ALBERTSEN, HANS ALBERSON, MARY GRODEN, JOANNA HEDGE, PHILIP J. JOSLYN, GEOFF KINVLER, KENNETH MARKHAM, ALEXANDER F. NAKAMURA, YUSUKE THILVERIS, ANDREW TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL CANCER IN HUMANS CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & Allegretti, LTD STREET: 1001 G Street, NW CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20001-4598 COMPUTER REANABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
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; TYPE: PRT
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US-09-125-635-12
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US-09-125-635-12
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APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
TITLE OF INVENTION: AIB1, A novel steriod receptor co-activator
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SEQ ID NO 12
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Patent No. 6562589
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/125,635
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 12
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                                 HSSNSHRNGSNRSPHSASPMLAAAV-----AQGGYSAGNSLLTSSSSSIQKMMASNIQR
                                                                    NRPLLRNSLDDLLGPPSNAEGQSDERALLDQLHTLLSNTDATGLEEIDRALGIPELVNQG
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                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/741,940
FILING DATE: 1922109
                TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
SEQUENCE CHARACTERISTICS
                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                   NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                        STATE: D.C
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                                                                                                                                                                                                                                                                                       USA
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THLIVERIS, ANDREW
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MARKHAM, ALEXANDER
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Query Match
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    DTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKY-RNYDRDSLVEA
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                                                                                                                                            GVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMP 1732
                                                                                                                                                                                      SHRNGSNRSPHSASPML----AAAVAQGGYSA-----
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                                                              KGKSHKPFRVKKIMDQVQQASASSSAPNKNQLD----
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Patent No. 564821
                                                                                                                 ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,548A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                               FILING DATE: 12
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 STREET:
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KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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HEDGE, PHILIP J.
                                                                                                                                                                                                                                                                                         USA
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Best Local Similarity
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Homo sapiens
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CLONE: APC
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                                        1673 GVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMP 1732
                                                                                                                                                                                                1555 TIDSEKDLIDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVY 161
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                                                                               SHRNGSNRSPHSASPML----AAAVAQGGYSA------
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                                                                                                                                                                                                                                                                                                                                                           AEKRESG-PKQ----AAVNAAVQR---VQVLPDADTLLHFATESTPDGFSCSSSLSALSL 1510
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                                                                                                                   KLLPSONRLOPOKHVSFTPGDDMPRVYCVEG--TPINFSTATSLSDLTIESPPNELAAGE 1672
                                                                                                                                                          K-IPSFKVSGPASSSSLSPGG-----LVGGHHPLNNNNSLSISN-----NSNHSSN
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    --MMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719
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19.3%; Pred. No. 6.1e-07;
1tive 179; Mismatches 511
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US-08-452-654-7
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                                                                         ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/452,654 FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: INHERITED AND SOMATIC MUTATITLE OF INVENTION: GENE IN COLORECTAL CANCER NUMBER OF SEQUENCES: 94
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1001 G Street, NW
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HEDGE, PHILIP J.
JOSLYN, GEOFF
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THLIVERIS, ANDREW
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CARLSON, MARY
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                                                            Version
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US-08-452-654-7
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TELEFAX: 202-508-72.

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 2842 amino acids
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
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STRANDEDNESS: si
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  K-IPSFKVSGPASSSSLSPGG-----LVGGHHHPLNNNNSLSISN-----NSNHSSN 624
                                              TIDSEKDLLDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVY 1614
                                                                                                    HVAAYRHRLPKSE---
                                                                                                                                              DEPFIQ-----KDVELRIMPPVQENDNGN----ETESEQPKESNENQEKEAEK 1554
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                                                                                               -----TPETNSSLDPNDA---SEDPIL 578
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; Sequence 7, Application US/08449731
; Patent No. 6413727
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
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                                                                                       TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1102
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                    CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGISLGSPFHLTPDQEEKPFTSNK------GPRILKPGEKSTLETKKIESES----- 2184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKAVQRGEM---SVHRAGSYYGVPH-----STLEYKVKERHLMRPRKREPKPQPDLV 827
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ZIP: 20001-4598
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                        GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-449-731-7
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7:
                                                                                                                1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/289,548 FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                      1358
                                                                                                                                                                                                                                                                                             1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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265; Conserv
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                                                                GEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLH--TLMLAAGIGAMPKLDETQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GA---TSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH
                       AEKRESG-PKQ----AAVNAAVQR----VQVLPDADTLLHFATESTPDGFSCSSSLSALSL 1510
                                                                                                              SEPCSGMVSGIISPSDLPDS--PGQTMPPSRSKTPPPPPQTAQTK-REV----PKNKAPT
                                                                                                                                                                                                   KSPSK-----SGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQ
                                                                                                                                                                                                                                             RAYSEEDLSRALQDVVANKLDARKSASQHHEQRS-ILDNRLFKMKHHD-------
                                                                                                                                                                                                                                                                                             AEDP-VSEVPAVSQHPRTK--
                                                                                                                                                                                                                                                                                                                                         AVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGR 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/449,731 FILING DATE: 25-May-1995 CLASSIFICATION: <Unknown>
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LENGTH: 2842 amino acids
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ilarity 19.3%;
Conservative 179
                                                                                                                                                        ---DELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGSDL 428
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Pred. No. 6.1e-07;
9; Mismatches 511;
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US-08-452-655B-2
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Patent No. 5783666
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  OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLK 2138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YADIKR----ERLSADS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVE---NVYDGIIRKTLQASEGNGSAAGNGSNGSNGHGHGHGHGHGHALLDQLLVKKTPL 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMP 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGISLGSPFHLTPDQEEKPFTSNK-----GPRILKPGEKSTLETKKIESES----- 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SASHINNNNSDLAHNKNKSGGGGGGGGGGGGTNGNGRSSRMTSRDDSETDASSFK 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQPKPI-LQKQSTFPQSSKDIPDRGAATDEKLQNF----AIENTPVCFSHNSSLSSLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGPQALSFQPNMFWPQTN-----ATNAYGLDFNRITEAMRN-PQASNHHGLMKSAQD 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHRNGSNRSPHSASPML----AAAVAQGGYSA-----GNSLLTSSSSSSIQ 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAATPNGLKLPLFE 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKY-RNYDRDSLVEA 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-----MMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKAVQRGEM---SVHRAGSYYGVPH-----STLEYKVKERHLMRPRKREPKPQPDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGKSHKPFRVKKIMDQVQQASASSSAPNKNQLD-
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                                                           ALBERTSEN, HANS
ANADIS, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
/ENTION: INHERITED AND SOMATIC MUTATIONS OF APC
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EQDHDGDELEDSNDDAEAEVDSNASTPVYPAE	KSPSKSGAQTPKSPPEHYVQETPLMFS	RAYSEEDLSRALQDVVANKLDARKSASQHHEQRS-	AVTPTTSEVSAAAISPALKDTPSDSVDAPLDLSSKPSPNSS	LYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQQ 	QHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLE	GATSTPSPPPBPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIH :	EDEPSQYNHS-SKEISQSNPNHCKTENHRLEQOHNGSQLLEEEDSENNQTSHDSSRTPTP	HISSYEISLERVAEECMGRRQWKHYQDKLTCSHLNIE-	3.7%; Score 221.5; DB 1; Similarity 19.3%; Pred. No. 6.1e-07; 5; Conservative 179; Mismatches 511;	INVENTION: GENE IN COLORECTAL CANCER SEQUENCES: 102 DENCE ADDRESS: 102 EE: Banner & Witcoff, Ltd. 1001 G Street, NW Washington D.C. 1001 G Street, NW RELEASE 1001 G STEMM: PC-DOS/MS-DOS 1001 G STEMM: NUMBER: US/08/452,655B DATE: 25-MAY-1995 1001 G STEMM: US 08/289,548 1001
FARAQLRKLSHLSEHNGSDL 428	RCTSVSSLDSFESRSIASSVQ 1406	ILDNRLFKMKHHDQ 376	318GDVKSVRACATFTPSGR 328 : :	QQQQQQQIAS 268	ASARATPAAATPANSLE 217 	JVAESAATATSSSTSNSHIH 164	SEEDSENNQTSHDSSRTPTP 107	EQQPIAIAGS 48 : : :	Length 2843; Indels 421; Gaps 63;	IN HUMANS

KĠIKĠĠKKVYKSL-ITĠKVRŚNŚEISGQMKQPLQANMPSIŚRGRTMIHIPĠVRNSŚ 2240	KGIKGGKKVYKSL-ITGKVRSN	2186	DЬ
DLNGGSSSSSHIKCESEAATGHHSPGHHTTS 1145	SGENGGQQNHKMMDLNGGSSSSSHIKCE	1102	8
DQEEKPFTSNKGPRILKPGEKSTLETKKIESES 2185	SGISLGSPFHLTPDQEEKPFTSNK	2140	DЪ
SASHINNNNSDLAHNKNKSGGGGGGGGGGUGQTNGNGRSSRMTSRDDSETDASSFK 1101	SASHINNNNSDLAHNKO	1048	8
LKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLK 2139	LKDIQRPDSEHGLSPDSENFDWI	2080	밁
SADS	YADIKRERLSADS	1027	δ
CFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLD 2079	CFSRNSSLSSLSIDSEDDLLQE	2020	Db
NDYAATCSSAS GESVKRSGSPMGN 1026	1	996	δλ
KET-EPPDSQGEPSKPQASGYAPKSFHVEDTPV 2019	IDQENNNKENEPIKET-EPPDSQGEP-	1975	DЪ
NVYDGIIRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGHGHALLDQLLVKKTPL 995	MVENVYDGIIRKTLOASEG	939	γQ
GQPKPI-LQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSD 1974	GQPKPI-LQKQSTFPQSSKDIP	1921	DЪ
WPQTNATNAYGLDENRITEAMRN-PQASNHHGLMKSAQD 938	AGPQALSFQPNMFWPQTN	888	γ
EKAELRKAKENKESEAKVTSHTELTSNQQSANKTQATAKQPINR 1920	EKAELRKAKENKESEA	1877	Дb
GLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAAAAATPNGLKLPLFE 887	GLTGPANKLQLDKLKAGPHGGSI	828	ş
-VRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSR 1876	VRGSFAFDSPHHYTPIEG	1834	탕
-SVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLV 827	VKAVQRGEMSVHRAGSYYG	779	Ş
TEYRTRVRKNADSKNULNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDR 1833	TEYRTRVRKNADSKUNLNAERV	1783	Db
DTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKY-RNYDRDSLVEA 778	DTSRFGASPNLLSQQHHSAHHL	720	Qy
MDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQN 1782	KGKSHKPFRVKKIMDQVQQASASSSAPNKNQLD-	1734	망
-MMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGT 719	KMMASNIQRQINEQSG	666	Ş
GVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMP 1733	GVRGGAQSGEFEKRDTIPTEGR	1674	Дb
SPMLAAAVAQGGYSAGNSLLTSSSSSIQ 665		625	δλ
KLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGE 1673	KLLPSQNRLQPQKHVSFTPGDDI	1616	DЬ
LVGGHHHPLNNNNSL	K-IPSFKVSGPASSSSLSPGG-	579	δ
TIDSEKDLLDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVY 1615	TIDSEKDLLDDSDDDDIEILEE	1556	DЬ
	HVAAYRHRLPKSE	547	Ş
KDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEK 1555	DEPFIQKDVEL	1512	Db
VGDFIKGLLVANSGGIMNEGLLNLLSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQ 546	VGDFIKGLLVANSGGIMNEGLLI	487	Ş
AAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSL 1511		1460	В
GEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQT 486	GEDVDRGSPKMGRHPACGNASAI	429	Ş
SEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTK-REVPKNKAPT 1459		1407	Дb

Search completed: October 29, 2003, 12:32:08 Job time : 45 secs

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E781 DROME
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T720 MOUSE
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APC HUMAN
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                                                                                                                                             InterPro; IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 2.
PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 2.
PROSITE; PS00633; BROMODOMAIN 1; 2.
PROSITE; PS50014; BROMODOMAIN 2; 2.
Developmental protein; Bromodomain;
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RESULT 1 FSH_DROME		45	44	43	42	41	40	39	38	37	36	35	34	
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		H	<u>, .</u>	Н	_	Н	_	Н	-	۳	Ļ	۳	ь	
	ALIGNMENTS	E2F_DROME	MN1 HUMAN	LUG_ARATH	SOL DROME	TCOF_HUMAN	APC_MOUSE	FTF1_DROME	YKZ6_CAEEL	E75C_DROME	YMJB CAEEL	E75A DROME	GAP_CAEEL	
			Q10571 homo sapien		P27398 drosophila			P33244 drosophila		P13055 drosophila		P17671 drosophila	P34288 caenorhabdi	

EMBL; M23221; AAA28540.1; -. EMBL; M23222; AAA28541.1; ALT_TERM. EMBL; M15762; AAA70423.1; -. EMBL; M15763; AAA70423.1; -. EMBL; M15763; AAA70422.1; -. EMBL; M15764; AAA70422.1; -. EMBL; M15764; AAA70422.1; -. EMBL; A43742; A43742. HSSP; Q92831; 1891. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). apparent membrane proteins."; Dev. Biol. 134.246-257(1989) -!- FUNCTION: REQUIRED WATERNALLY FOR PROPER EXPRESSION OF OTHER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX. -!- SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN. -!- SIMILARITY: Contains 2 bromodomains. -!- SIMILARITY: Contains 1 ET domain. Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227; FSH_DROME STANDARD; PRT; 2038 AA. p13709; p13710; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Female sterile homeotic protein (Fragile-chorion membrane protein). FS(1)H OR FSH. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way MEDLINE=89276730; PubMed=2567251; Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.; "The Drosophila fish locus, a maternal effect homeotic gene, encodes apparent membrane proteins."; FlyBase; FBgn0004656; SEQUENCE FROM N.A. fs(1)h. ormatics and the EMBL outstation There are no restrictions on it as its content is in no warms as its content is in no warms.

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123 567 1106 350 471 770

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BROMODOMAIN_1; 2.
BROMODOMAIN_2; 2.
tein; Bromodomain; Transmembrane; Repeat.

EAMRNPQ 925 AAEKEQ 1708	2PQTNATNAYGLDFNRITE :: ::	902 1649	B 8
NMFW 901 : SWSSL 1648	PHGGSKLSNALKNQNNQAAAAAAAAAAAAATPNGLKLPLFEAGPQALSFQP	845 1601	용 성
LDK-LKAG 844 :	VPHSTLEYKVKERHLMRPRKRE	798 1549	음 성
VHRAGSYYG 797	AHHLTHQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMS	738 1529	음 성
LSQQHHS 737 -QQQQHQ 1528	B EQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHS	678 1514	용성
QKYMASNIQRQIN 677 : : : : QQMQQMQLQQQHH 1513	HRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSI	. 1467	B 8
SSNS 625 : QQQQQQA 1466	NDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNH- :: : : :: : DYVTELLSKGAENVGGNNGNHLLNFNLDMAAAYQQKHP	570 1422	B 8
TNSSLDP 569	ASQENSNGNASLLLQQQQHQQHHQQHQQQQQQQHVAAYRHRLPKSETPE	513 1378	유
LL-NLLS 512 	DANVLLHTLMLAAGIGAMPKLDETQTVGDPIKGLLVANSGGIMNEG	461 1324	g 8
PASI-PL 460 : NNNANPL 1323	1RAQLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASI-P 	411 1269	B 8
410 SQSSGGI 1268	S NRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFA	366 1228	ß &
EQRSILD 365	7 NSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDV-VANKLDARKSASQHHE	307 1192	B 8
SSKPS-P 306 ::	3 QQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKP 	258 1142	유 성
NLINSLASQ 257 :: vvmGGNLPS- 1141	AASARATPAAATPANSLELYKLLTQRAAKVTSMDSMAAQLAQFSLLADF	200 1111	유성
NRARHIA 199 : DGDE 1110	NAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSG 	140 1064	ß 8
Gaps 50;	1 5.2%; Score 311.5; DB 1; Length 2038; Similarity 21.1%; Pred. No. 1.7e-07; 86; Conservative 129; Mismatches 331; Indels 425;	ery Match st Local tches 23	Ma Ma
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RX MEDLINE-2019(6006; PubMed=10731132;
RX MEDLINE-2019(6006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley S.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bookson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merikolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menson D.R., Pettman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rienert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Sense H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88232956; PubMed=2897632; Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.; Blochlinger K., Edmer R., Jack J., Jan L.Y., Jan Y.N.; "Primary structure and expression of a product from cut, a locuinvolved in specifying sensory organ identity in Drosophila."; Nature 333:629-635(1988).
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CT OR CG11387.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
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TRANSFAC; T02004; -.

R FlyBase; FBgn0004198; ct.

R GO; GO:0005634; C:nucleus; IDA.

R GO; GO:0008587; P:wing margin morphogenesis; NAS.

JR GO:FRO0108587; P:wing margin morphogenesis; NAS.

JR InterPro; IPR001015; Cut.

DR InterPro; IPR001350; Hmoeo CUT.

DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00276; CUT; 3.

DR Pfam; PF00046; homeobox; 1.

DR Pfam; PF00046; homeobox; 1.

DR ProDom; PD000010; Homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

-i- FUNCTION: Regulator of cell fate decisions in multiple lineages. Specifically, functions as a determination factor that specifies sensory organ identity in precursor cells probably also involved in cell type specification of Malpighian tubules. In absence of cut gene external sensory organs are transformed into chordotonal
                                                                                                                                                                                               DNA_BIND
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DNA_BIND
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                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Transcription regulation; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X07985; CAA30794.1; -.
EMBL; AE003441; AAF46264.2; -.
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SIMILARITY: BELONGS TO THE CUT HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE: CELL-SPECIFIC PATTERN OF EXPRESSION. BROADLY EXPRESSED DURING EMBRYONIC DEVELOPMENT.

DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (Probable).
TISSUE SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S03170;
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798
1056
1329
1463
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                                                                                                                                                                                                                                                                                       regulation; Homeobox; DNA-binding;
protein; Nuclear protein; Repeat; Coiled coil.
65 343 COILED COIL (POTENTIAL).
33 499 COILED COIL (POTENTIAL).
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1161
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1522
1695
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   ¥.
                           ASN-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ALA-RICH.
HIS/GLN-RICH (OPA-REPEAT
ALA-RICH.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
CUT 1.
COILED COIL (POTENTIAL).
CUT 2.
CUILED COIL (POTENTIAL).
               ALA/PRO-RICH
                                                                                                                                          ALA-RICH.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                              ALA/GLN-RICH.
                                                                                                                                                                                               HOMEOBOX
 08BF80C4861BD0AB CRC64;
                                                                                                                                                                                                                                                            COIL (POTENTIAL).
                                                              (OPA-REPEAT) .
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 Qy	Db	У	Db	Qy	da	Q Q	Db Qy	Dδ	Qy	Db	Qy	Db	Qγ	מם	δ	рь	Q	מם	γQ	Dъ	Qy	ф	γ	Db	Qy Qy	Dъ	Qy	ФФ	γQ	ФФ	γQ	DЪ	Q	Quer Best Mato
947 IIRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGHALLDQLLVKKTP 994	1042 KVENQLKQHQHLNPEQAAAQQREREREQREREQQQRLRHDDQDKMARLYQE 1092	887 EAGPQALSFQPNNFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDG 946	985 SMSEDRIAHILSEASSLMKQSSVAQHREQERRSHGGEDSHSNEDSKSPPQSCTSPFF 1041	835 KLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAAAAAAAAAATPNGLKLPLF 886	925 LSKPKPWDKLTEKGRDSYRKMHAWACDDNAVMLLKSLIPKKDSGLPQYAGRGAGGAGGDD 984	806KVKERHLMRPRKRE	753 QEALGKGTRPKKGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEY- 805	GFLPGLPAFQFAAAQVAAGGDGRGHYRFADSELQLPPGASMAGRLGES	SSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSA	770 QLAASLASTLNGTKSLMQEDSNGLAAVAMAAHAQHAAALGP 810	3GYSAG	716GHHLHGHGLLHPSSAHHLHHQTTESNSNSSTPTAAGNNNGSNNSSSNTNANSTA 769	596 PGGLVGGHH	676 HQHQQQHHQQQHLHQQHHHHLQQQPNSGSNSNPASNDHHH 715	536 QQHHQQQQQQHVAAYRHRLPKSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLS 595	623 AAAAAACANDPNKF-QALLIERTKALAAEALKNGASDALSEDAHHQQQQHHQQQ 675	477 AMPKLDETQTVGDFIKGLLVANSGGIMNEGLLNLLS-ASQENSNGNASLLLQQQQHQQHH 535	601 EQHSPLDLNVLSPNSAIAAAAA 622	417 LSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIG-476	552 DEDQAMLVDSEEAEDKPEDSHHDDDEDEDEDREAVNATTTDSNELKIKK 600	357 HHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYFAEFARAQLRK 416	520 LNTAAERPMDASSNADLPESTKAPVPAEDDEE 551	298 LDLSSKPSPNSSISGDV-KSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQ 356	465 RLEEHLEVKROHIIRLEARLDKOQINEALAEATALSAAASTNNNNNSQSSDNNKK 519	244 LLADFNLINSLASQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAP 297	425 NNNNGQPAVLLAAKDKEIKALLDELQRLRAQEQTHLVQIQ 464	188 NNSSGNRARHIAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFS 243	365 GGNESEQHVASSAEDDDCANNNTNTSNNNNTSNTATSNTNNNNNNNNSSSGNSEKRKKKNN 424	138 TVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSN 187	320 TQQQHQQQDTEDLEENKDAGEASLNVSNNHNTTDSNNSCSRKNNN 364	78 EQQHNGSQLLEEEDSENNQTSHDSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLL 137	269 HQDEEELDDEEEDEEEDEDEDEDEENASMQSNADDMELDAQQETRTEPSAT 319	26 YQDKLTCSHLNIEEQQPIAIAGSEDEPSQYNHSSKEISQSNPNHCKTENHRL 77	Query Match 5.0%; Score 299.5; DB 1; Length 2175; Best Local Similarity 19.7%; Pred. No. 6.7e-07; Matches 256; Conservative 167; Mismatches 491; Indels 383; Gaps 52;

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Rango Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Relson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Relson C.R., Miklos G.L.G.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Meishov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bunched protein, class 2/class 3 isoforms (Shortsighted protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treisman J.E., Lai Z.-C., Rubin G.M.; "Shortsighted acts in the decapentaplegic pathway in Drosophila eye development and has homology to a mouse TGF-beta-responsive gene."; Development 121:2835-2845(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96038094; PubMed=7555710;
Treisman J.E., Lai Z.-C., Rubin G.M.;
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                RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
"The genome sequence of the development and for a nervous system morphogenesis, be development and oogenesis. May be required for the transmission of the dpp signal and for a the second optic lobe relative to the first. Plays a role in the second optic lobe relative to the first. Plays a role in the second optic lobe relative to the first. Plays a role in the second optic lobe relative to the first. Plays a role in the second optic lobe relative to the first. Plays a role in the second optic lobe relative to the first.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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            DOMAIN
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EMBL; AE003336; AAF53200.1; ALT_SEQ
EMBL; AE003636; AAF53201.1; ALT_SEQ
EMBL; AE003636; AAF53201.1; ALT_SEQ
PIR; T13804; T13804.
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DOMAIN
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ProDom; PD007152; TSC-22_Dip_Bun; 1.
PROSITE; PS01289; TSC22; 1.
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InterPro; IPR000580; TSC-22_Dip_Bun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q24523-2; Sequence=VSP_006670; SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY. CAUTION: Ref.2 sequence differs from that shown due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the dorsal appendages.
SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining proper dorsal cell fates leading to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPTPGATSTPSPPPE--PIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAAT--ATSSSTS
     TPQAAPTFAAVAAGQSPNFQLEQQQQQQQATSQIDGIVPQPFNPQQQQQQTPQQSTAQQA
                               L-AAAVAQGGYSAGNSLLTSSSSSIQKMMASN----IQRQINEQSGQESLRNGNVSDCS
                                                                                 VSGPASSSSLSPGG--LVGGHHHPLNNNNSLSISNNSNHSSNSH--RNGSNRSPHSASPM
                                                                                                                                              AAYRHRLPKSETPETNSSLDPNDASE---
                                                                                                                                                                           QQQQQQQQTIVGNALTKTLPVALRNVSRSSSVTRSPNATVEFLSPNLLAQQQQQQQQL
                                                                                                                                                                                                     GAAGVGAGSEAPAHKTTQS----MILPPTQKLNE---NHLEANSTDANWNYAEQQQ
                                                                                                                                                                                                                                                                                          TQHRSERFKVVKIESTEPFKRGRWMCMDYLDHSSVGNGGNNNEKTGSSTSEAHAAT-TDG
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                                                              - PGAGGYANYONGGDSAVGA----ASNNNSAAAATGESQLSTSYVEQQQQQQQPLSPAPL
                                                                                                                    -----FDSVNANAASSPNPAGDPNNMDYARTAAMQLHQTLQQLKQREDAMDVP---
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7%; Pred. No. 1.5e-06;
143; Mismatches 423;
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> QQQ (IN REF. 1)
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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang, Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HR38 DROME STANDARD; PRT; 1073 AA. P49869; O18383; O9VIK4; O1-CCT-1996 (Rel. 34, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Probable nuclear hormone receptor HR38 (dHR38) HR38 OR NR4A4 OR CG1864.
                                                                                                                                                                                                                                                                                                         MEDLINE=98370123; PubMed=9704500; Komonyi O., Mink M., Csiha J., Maroy P.; "Genomic organization of DHR38 gene in D: Alu-like repeat in a translated exon and development.";
                                                                                                                                                                                                                                                                                                                                                                                                       Sutherland J.D., Kozlova T., Tzertzinis G., Kafatos "Drosophila hormone receptor 38: a second partner for suggests an unexpected role for nuclear receptors of factor-induced protein B type.";
Proc. Natl. Acad. Sci. U.S.A. 92:7966-7970(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                            "Drosophila hormone receptor adult cuticle formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DROME
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                    Kozlova T., Pokholkova G.V. Zhimulev I.F., Kafatos F.C.
                                                                                                                                                                                                                                  MEDLINE=98315108; PubMed=9649534;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Arch. Insect Biochem. Physiol. 38:185-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutherland J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95372400; PubMed=7644522;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Ra de Pablos R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Houland T.J., Wei M.-H., Ibegwam C., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Ra Harris E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Williams S.M., Woolsey K., Venter E., Wang A.H., Wang X., Ra Yurskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ra Yurskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ra Yurskas R., Tector C., Turner R., Venter S., Zhu S., Zhu X., Smith H.O., The Genome Sequence of Drosophila melanogaster.";
EMBL;
EMBL;
EMBL;
                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation, regulation, and DNA-binding properties of three Drosophila nuclear hormone receptor superfamily members."; Proc. Natl. Acad. Sci. U.S.A. 92:10604-10608 (1995).
-i- FUNCTION: BINDS TO NGFI-B RESPONSE ELEMENTS. PLAYS AN IN ROLE IN LATE STAGES OF EPIDERMAL METAMORPHOSIS.
-i- SUBUNIT: FORMS A HETERODIMER WITH USP.
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                                                                                                                                or send
                                                                                                                                                       entities requires
                                                                                                                                                                           modified
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DEVELOPMENTAL STAGE: LOW LEVELS IN 0-8 HOUR EMBRYOS AND ADULTS.
HIGHER IN LATE EMBRYOGENESIS AND DURING LARVAL AND PUPAL STAGES
SHORT ISOFORM IS ENRICHED IN PUPAE AND ADULTS, LONG ISOFORM IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P49869-2; Sequence=VSP 003714;
TISSUE SPECIFICITY: UBIQUITOUSIY EXPRESSED IN PREBLASTODERM
EMBRYOS, SPECIFICALLY IN CENTRAL NERVOUS SYSTEM AND INTESTINAL
TRACT. HIGHLY EXPRESSED IN THIRD INSTAR LARVAL IMAGINAL DISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                              SIMILARITY:
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                                                                                                                                                                                                                                                                                                          subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                  à
                    AJ002073; CAA05172.1; -. AE003667; AAF53914.1; -.
                                                                 X89246; CAA61534.1; -.
Y15606; CAA75690.1; -.
  U36762; AAC46926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P49869-1;
                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                     non-profit institutions as long as and this statement is not removed. Urequires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                            Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                          to the nuclear hormone receptor family. NR4
                                                                                                                                                  oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                           is produced through a collaboration
                                                                                                                                                                                             There are no restrictions ng as its content is in
                                                                                                                                                                                                                                      and the
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PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000536; Horn
InterPro; IPR001723; Stdl
InterPro; IPR001628; Znf
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FlyBase; FBgn0014859;
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                                                                                                                                                                                                                                                 255
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                                                         OHH----NHLLHQQHHNQQQQQQQQQQQQQQQQQDHLQQQHQQQLVSPQQHLLKSETL
                                                                                                                                                                                                                                                                                                                          SARATPAAATP----
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LSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLA----
                                                                                                                              LLQPNSSFSSLSPFDNFSTQTASTTTTTS-----
                                                                                                                                                                                                                                             ASQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKP-
                                                                                                                                                                                                                                                                                       ALTPAPPATEPRKIKPLGAGKLKVGK-TDSNSDSNSNCDSRAAAAASTS
                                                                                                                                                                                                                                                                                                                                                                                                     QGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAA
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                                                                                           EQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAE---VDSNASTPVYPAEFARAQLRK
                                                                                                                                                                    --SPNSSISG----DVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00031; NUCLEAR_RECEPTOR; 1.
Transcription regulation; DNA-binding; Nuclear protein;
er; Alternative splicing; Developmental protein.
744 809 NUCLEAR RECEPTOR-TYPE.
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//Y-ALA.
//SING (in iso.
//FIId=VSP 003714.
//FIId=VSP 003714.
// -> VSSPSV (IN P
S -> L (IN REF.
STAQ -> LHGER
// A -> D (IN P
102 N -> S (IN
1041 S -> R
105 N -> D
106 N -> D
107 N -> D
108 N -> D
109 N -> D
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Stdhrmn_receptor.
Znf_C4steroid.
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                                                                                                                                                                                                                                                                                                                          -ANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSL
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Pred. No. 5.6
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Q -> LHGER (IN REF.
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> S (IN REF. 2).
> R (IN REF. 2).
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XX MEDLINE=20196006; PubMed=10731132;
XX MEDLINE=20196006; PubMed=10731132;
XA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
XA Adams M.D., Celniker S.E., Hi P.W., Hoskins R.A., Galle R.F.,
XA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
XA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
XA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeifer B.D.,
XA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
XA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
XA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
XA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
XA Ballew R.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
XA Ballew R.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
XA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
XA Borkova D., Botchan M.R., Bouck J., Brostein P., Brottier P.,
XA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
XA Genry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
XA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
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STANDARD; PRT; 1669 AA.
Q9V727; 076930;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Polycomb protein Asx (Additional sex combs).
ASX OR CGB787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 125:1207-1216(1998)
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Additional sex combs gene of Drosophila encodes ein that binds to shared and unique Polycomb grou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TaxID=7227;
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INTERACTION WITH TAN
MEDLINE=21290825; PubMed=11397012;
MEDLINE=21290825; PubMed=11397012;
MEDLINE=21290825; PubMed=11397012;
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Milne T.A., Brock H.W., Krause H.M.
"Tantalus, a novel ASX-interacting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Atypical Polycomb group protein, which may be involved in both Polycomb group (PCG) and trithorax group (trXG) complexes. PCG and trXG proteins act by forming multiprotein complexes, which are respectively required to maintain the transcriptionally repressive and transcriptionally active state of homeotic genes throughout development. PCG and trXG protein complexes are not required to initiate repression and activation, but to maintain it during later stages of development. Both complexes probably act the methylation of histones, rendering chromatin heritably changed the stages of the complexes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with Tan. SUBCELLULAR LOCATION: Nuclear; associated with chromatin.
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deposited

Colocalizes with many PCG sites on polytene chromosomes. It also associates with many unique sites on polytene chromosomes.

FISSUE SPECIFICITY: Highly expressed in nurse cells and deposited in occytes late in cogenesis. Ubiquitous in early embryos. Late embryos show higher levels in CNS and neurectoderm.

DEVELOPMENTAL STAGE: Expressed both maternally and zygotically. Early embryos have high levels of expression, this drops off and zygotic expression begins at 3-6 hour embryos. Expression levels are low in larvae and medium in pupae and adults.

DOMAIN: Contains two Leu-Xaa-Xaa-Leu-Leu (LXXLL) motifs, which may be required for an association with nuclear receptors (By similarity).

SIMILARITY: Belongs to the Asx family.

CAUTION: Ref. 1 sequence differs from that shown due to frameshifts in positions 608 and 719.

entities or send a use by non-profit institute modified and this statement entities requires a license This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation European an email to license@isb-sib.ch) Bioinformatics Institute. The profit institutions as long agreement is not removed. (See http://www.isb-sib.ch/announce, There are no restrictions ng as its content is in Usage ş and a collaboration for commercia ö 9

EMBL; AJ001164; CAA04568.1; ALT_FRAME EMBL; AE003814; AAF58239.1; -.

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                                                                                                                                                                                                                                                                                       SISGDVKSVRACATPTPSG--RRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDN
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                                                                                                          EGLLNLLSASQENSNGNASLLLQQ-----
                                                                                                                                                                                                YPAEFARAQLRKLSHLSEHN------
                                                                                                                                                                                                                                           RLFKMKHHDQEQDHD-GDELEDSND------DAEA-----EVDSNASTPV
                                                                                                                                                                                                                                                                                                             TVAKLQQQQQ-
                                                                                                                                                                                                                                                                                                                                                                           NRARHIAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPEALAPNPDVANQFVSYLQNVELAAETKAPLDNSNEADITTGTNSHDFVFSDTIDHAYF
EQHQQQATAQQKHQQIQQFALQQAQLHQRQLLAQ---AANNNLLQQQQQQQQQNVALPTTQ 1126
                    SISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKM-----M
                                                               RLPKSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHPLNNNNSL
                                                                                                                                  NSNDSSN---
                                                                                                                                                     NQGAPASIPLDANVLLHTLMLAAGIGAMP-----KLDETQTVGDFIKGLLVANSGGIMN
                                                                                                                                                                           QQQHHQQLHIQDVVQLAQHSFMPQAHSEFGNDIGQEMLCDAVPMSAAEMEVSSTVITNSS
                                                                                                                                                                                                                       IMHNDVCHDVLGDEDEGDQEEDEDDEVVECMTEEQQLIDEDSEAVREIVDKLQQHQQQQN
                                                                                                                                                                                                                                                                 WNFGDIK----LSSSQSSGDQQRNLSHEAID--LMDVV------QDADVIDD
                                                                                                                                                                                                                                                                                                                                                                                                  ----CTSSSSSASMS---SSCSSSNSGSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              QEH----QSTINHNFFTSSSSSNTATTAANKLEEHSDKPEDSPLPI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQHNGSQLLEEEDSENNQTSHDSSRTPTPGA----TSTPSPPPEPIDWRPSAKCNFCV
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129
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228
                                                                                   -QQQRQQQQQLLQQFTLQAAAAQQQQQQQQQQQQQQQQQQQQQQATSSNSLGK 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
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                                                                                                                              -NISLCSSTNSLTINQMPHQASQQPQQNAQSNAQQQRQILVDSNGQIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
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POLY-THR.
POLY-HIS.
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ALA-RICH.
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 272.5;
Pred. No. 9.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K -> N (IN REF. 1).
S -> T (IN REF. 1).
MISSING (IN REF. 1).
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LXXLL MOTIF 2.
SQ -> CE (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLN
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HHHHHEMQQQQQHQQPQPLGNVGAAANIVRRNIAA 1554
                                                                                                                                                                                                                                                                                                                                                                           ILNOHOPTTTTAPAPINPVTLN---VSTVAATPMSNITTATGSMAAAVAAAPPONVLKOE 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKFIAKPLNIIS----MTRPANASPTTAATTANTASI----PS-AYANVVAVTGAQQQQSP
                                  SFKSGENGGOONHKMMDLNGGSSSSSHIKCESEAA 1133
                                                                                                            SSDEEHSASHINNNNSDLAHNKNKSGGG---GGGGGNGQTNGNGRSSRMTSRDDSETDAS 1098
                                                                                                                                                                                     HALLDQLLVKKTPLPFTNHRNNDYAATCSSASGESVKRSGSPMGNYADIKRERLSADSGG 1041
                                                                                                                                                                                                                                                                                                   ELLVSGAVGAGALPAGLPPNVMGVG-----RPGVYKVIGPRMSG-----FPRKKYVQ 138:
                                                                                                                                                                                                                                                                                                                                                                                                              ---KPQPDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAAAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASNIQRQINEQSGQESLRNGNVS-DCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGAS
                                                                         QAPRASSAPPMHQNQFVTVQNPLHSINGIPMGGRGRPASVDTTAGSGNVIAPPISATDAL 1519
                                                                                                                                                                                                                                                             RNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHG
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                                                                                                                                                                                                                                                                                                                                  ----AAAAAAATPNGLKLPLFEAGPQALSFQPNMF---WPQTNATNAYGLDFNRITEAM
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                                                                                                                                                  ----TTSPVPVQNPQ-----QPAPEQLIHQNGN--GQYVLVHRANVGA-ADN 1.459
                                                                                                                                                                                                                          -SPTTLIRHVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LPPGAVNLERS---YQICQAVIQ-NSPNRENLKAQLRPPAA 1279
                                                                                                                                                                                                                          -SPGPGGATATAQQLQMLQQHHQS----
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RESULT 6
SUZ2_DROME
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SEQUENCE FROM N.A.
STRAIN=Canton-S;
STRAIN=91279476; PubMed=2057369;
Brunk B.P., Adler P.N.;
Brunk B.P., Adler P.N.;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Suppressor 2 of zeste protein (Protein post
SU(Z)2.
                                                                                                                                                                                         WITH OTHER FROLEDING.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                      Nucleic Acids Res. 19:3149-3149(1991).
-!- FUNCTION: REGULATES EXPRESSION OF THE HOMEOTIC SELECTOR GENES BY INFLUENCING HIGHER-ORDER CHROMATIN STRUCTURE THROUGH INTERACTION WITH OTHER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUZ2_DROME
P25172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
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era; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                             gene
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Query Match
Best Local S
Matches 246
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InterPro; IPR001841; Znf ring.
Pfam; PPF00097; zf-C31C4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS00089; ZF RING 2; 1.
Zinc-finger; Developmental protein; DNA-b; ZN_FING 35 74 RING-TYPE.
DOMAIN 623 628 POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc-finger;
ZN FING
DOMAIN 6
DOMAIN 10
DOMAIN 12
CONFLICT 7
CONFLICT 7
CONFLICT 8
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EMBL; X56799; CAA40135.1;
PIR; S14871; S14871.
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        658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                               TAK-PNHKLDFKRSHSLASGELDLQKL---KLDSTSTSEALNR---TLGEEARSINSL
                                                                  --HHPLNNNNSLSISNNSNH----SSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLL
                                                                                                                                  DPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGH-----
                                                                                                                                                                                                                                VVGGAPTPPPTT------AEPEQQQQQQ------
                                                                                                                                                                                                                                                                  ANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLN
                                                                                                                                                                                                                                                                                                                                   SNASTPVYPAEFARA-----QLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNAS
                                                                                                                                                                                                                                                                                                                                                                                             VVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELE-----DSNDDAEAEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                   ETYAKNIGLKPIEQPLQQSAS-NPDSKYSPNASPMSSCSSSTNGSSSSLGTADASTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SL--RSNDMRYSDYAVSKVKSEPEQEQFLLPREREQQPLEANTNIVVSIPPSQLRKSYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTQRAAKMTSMDSMAAQL-------AQFSLLADFNLINSLASQQQQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEIDSGSPRSKVRCKTPPKVSPSSKNKRLTSSKR------EAEPESPVSNFK
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                                   PAKPPLSSNNNR--KPNSGHFAVPQAPTHRNMYHMQRYQSTPSSIA-----SAANKMP
                                                                                                                                                                                                 LLSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQQHVAAYRHRLPKSE--TPETNSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEDFELKTANRKGVGHLPKLKIELNSMKSKLSMPLSA---GPRLEDTSCSSSCSAQQLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQD
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                                                                                                   -LFKAYTP-STTPTAPHTVAGGKPKQQQQQMPQQPQAVLQQSMAKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154;
      -SIQKMMASNIQRQINEQSGQES----
                                                                                                                                                                oddopododddddddrvv----LpkIkDLTLpTsppL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN REF. 1; CAA40134).

K -> N (IN REF. 1; CAA40134).

A -> R (IN REF. 1; CAA40134).

MISSING (IN REF. 1; CAA40134).

D -> E (IN REF. 1; CAA40134).

MISSING (IN REF. 1; CAA40134).

A -> P (IN REF. 1; CAA40134).
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POLY-SER.
MISSING (IN REF. 1
K -> N (IN REF. 1
A -> R (IN REF. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 271; DB 1;
Pred. No. 8.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398;
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     -- LRNGNVSDC
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                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                            MEDLINE=95021209; PubMed=7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
Mevel-Ninio M.T.M., Terracol R., Kafatos F.C.;
"The ovo gene of Drosophila encodes a zinc finger protein required for female germ line development.";

EMBO J. 10:2259-2266(1991).

-i- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-i- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                               STRAIN=Oregon-R;
MEDLINE=91293102; PubMed=1712294;
                                                                                                                                                                                                                                                                    TISSUE=Ovary;
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc_finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0003028; ovo.
InterPro; IPR007087; Znf_C2F
Pfam; PF00096; Zf-C2H2; 3
SMART; SM00355; ZnF_C2H2; 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DUTRING COGENESIS. STORED IN THE PACTUMULATES IN THE EMBRYOS EXCEPT FOR ITS CONTINUED BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

SIMILARITY: Contains 4 C2H2-type zinc fingers.
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                              TPTTSEVSAAAISPALKDTPSPSVDAPLDL-SSKPSPNSSISGDVKSVRACATPTPSGRR
            MGSSGQFNASAYEDAIMS--
                                                                         TPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQQIASAV
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                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
SEQUENCE
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RA Abril J.F., Moyle C., Bakel B.G., Mell G., Welbul C.K., MALLUS G.L.S., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Bellew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Benos P., Baroktier P., RA Burtis K.C., Busam D.A., Buller H., Gadeu E., Center A., Chandra I., RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Bocchan M.R., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocka S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocka S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.R., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.R., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris M.R., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Liu X., Mattei B., McIntosh T.C., Kraytiz S., Kulp D., Lai Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Lasko P., Lei Y., Lumphy B., Murphy L., Muzny D.M., Nelson D.L., Moharris J., Moshrefi A., RA Mount S.M., My M., Murphy L., Muzny D.M., Nelson D.L., RA Rainert K., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Milliams S.M., Woodage T., Weinstock G.M., Meinschae F., Smith T., RA Palazzolo M., Sunders R.D.C., Scheeler F., Shen H., Ra Mang X., Wang S., Land G., Zhong G., Zhong L., Wang S., Zhon M., Zhong G., Zho Q., Zheng L., Friede M., Woodag
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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"The Drosophila gene Hairless encodes a novel basic protein that controls alternative cell fates in adult sensory organ development.";
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v. 38:143-162/1702.
                                                                                                                                                                  =No experimental confirmation available;
SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
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GO; GO:0003714; F:transcription co-repressor activity; IDA.
GO; GO:0007219; P:N receptor signaling pathway; NAS.
GO; GO:0008052; P:sensory organ determination; IMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                        FSDDNSSIQSSPWQRDQPWKQSRPRRGISKELSLFFHRPRNSTLGRAALRTAARKRRRP-
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ory organ determination, IMP.
Nuclear protein; DNA-hinding.
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S -> A (IN REF. 2).
S -> F (IN REF. 3).
OH -> LL (IN REF. 2).
A -> R (IN REF. 2).
A -> R (IN REF. 2).
ANDA -> RLLP (IN REF. 2).
ANDA -> RLLP (IN REF. 2).
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MEDLINE=20503946; PubMed=11051550;

MEDLINE=20503946; PubMed=11051550;

Xu C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.;

"Overlapping activators and repressors delimit transcriptional

"Overlapping activators and repressors delimit transcriptional

response to receptor tyrosine kinase signals in the Drosophila

response to receptor tyrosine kinase signals in the Drosophila

cell 103:87-97(2000).
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Bukaryota, Metazoa, Arthropoda, Brachycera,
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                         Drosophila virilis (Fruit fly)
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FUNCTION: Required for proper neuronal differentiation of most or all neurons and their precursors in central and peripheral nervous systems, axonal outgrowth and pathfinding. Not required for the
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(Rel. 41, Last ann
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SUBCELLULAR LOCATION: Nuclear (By similarity)
SIMILARITY: BELONGS TO THE PROSERO HOMEOBOX
SIMILARITY: Contains 1 homeobox domain.
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   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Best Local Sim
Matches 210;
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EMBL; Z71330; CAA95525.1; -.

PIR; S62982; S62982

SGD; S0004999; VAC7.

GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0000324; C:vacuole (sensu Fungi); IDA.

GO; GO:0000324; F:enzyme regulator activity; IGI.

GO; GO:000012; P:phospholipid metabolism; IGI.

GO; GO:000011; P:vacuole inheritance; IMP.

Hypothetical protein.

SEQUENCE 1165 AA; 128140 MW; 0414978AA3066CE7
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"The sequence of a 44 420 bp fragment located on the left chromosome XIV from Saccharomyces cerevisiae.";
Yeast 11:967-974(1995).
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SEQUENCE FROM N.A.
STRAIN-S288c / FY1676;
MEDLINE-96021608; PubMed-8533472;
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Yeast 12:297-297(1996).
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                   526
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L---QQQQHQQHHQQQHQQQQQQHVAAYRHRLPKSETPETNSSLDPNDASEDPILKIPS
                                                        AINDDSHESNSEKPTKADFFAARLATAVGE
                                                                                                                                                                                                                             QDHWH-SDINRAGTSMSTSDIPTDLHLEHIGSVSSTNNNSNNALINHNPLSSHLSNPSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIHOHDSDSN-----SSASLP----HHISSSSSSNNNSSGNRARHIAAASARATPA--
                                                                                                                            ADNHINN ------KKKTSSNNNGNNSNSASNKTNADI KNSNADLSASTSNNN
                                                                                                                                                                   LSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMP
                                                                                                                                                                                                        DDNENNNKKKKKNKNINSGKNERNDDTSKICTTSTKTAPSTAPLGSTDNTQALTASVSSSN
                                                                                                                                                                                                                                                                                                                     VRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQ
                                                                                                                                                                                                                                                                                                                                                        SKAFRKASAFSNNTAPSTSNNIGSNTPP-----APL----LPLPSLSQQNKPKI
                                                                                                                                                                                                                                                                                                                                                                                           QQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AATP--ANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLAS
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                                                                                         ETQTVGDFIKGLLVANSGGIMNEGLLNLLSASQEN-----SNGNASLL
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Pred. No. 8.1e-05
8; Mismatches 39
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                                                      NEISDSEETFVYESAANSTKNLI
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RESULT 11
BRC4_DROMI
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BRC4_DROME STATULES

G242706; O46064; O9W575;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2010 (Rel. 42, Last annotation update)

15-SEP-2010 (Rel. 42, Last annotation update)

16-OCT-2001 (Rel. 42, Last annotation update)

17-2-Complex core-protein isoform 6.
MEDLINE=20196011; PubMed=10731137;

MEDLINE=20196011; PubMed=10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Panadoiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                Bayer C.A., Holley B., Fristrom J.W.;
Bayer C.A., Holley B., Fristrom J.W.;
"A switch in broad-complex zinc-finger isoform expression is bosttranscriptionally during the metamorphosis of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                        STRAIN=Oregon-R;
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                           MEDLINE=96299417; PubMed=8660872
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Imaginal disks,
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M.C., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M.C., Pfeiffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova S., Delcher A., Deng Z., May/R.D., Dew I., Dietz S.M., A depablos B., Delcher A., Deng Z., May/R.D., Dew I., Dietz S.M., Ra Golosh K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra de pablos B., Carley S., Dahlke C., Davenport L.B., Davies P., Ra de pablos R., Bortelian A.E., Garg N.S., Gelabatt W.M., Glasser K., Ra Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvis N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X., Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Mcimel B.E., Kodira C.D., Fort C., McLeod M.P., McPherson D.L., Ra Kimel B.E., Kodira C.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Mcimel B.E., Kodira C.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Mcimel S.P., Liang S.M., Nusokerin D.R., McShrefi A., Wonter E.N., Smith T.T., Shen H., Smith T., Shen H., Shith T., Shen 
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                                                                                                                                                                                                                                                                                                                                                                   Drosophila metamorphosis.";
Dev. Biol. 187:267-282(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                 demonstrate functional redundancy
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97384928; PubMed=9242423;
Bayer C.A., von Kalm L., Fristrom J.W.;
"Relationships between protein isoforms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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Science 287:2220-2222(2000).
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IsoId=Q24206-1; Sequence=Displayed;
Name=1; Synonyms=BCORE-TWT1-Q1-Z1;
IsoId=Q01295-1; Sequence=External;
                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
Event=Alternative splicing;
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                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION OF SALIVARY GLAND
                                                                                                       ime=2; Synonyms=BCORE-Q1-Z1;
IsoId=Q01295-2; Sequence=Ex
                                                            IsoId=Q01295-3;
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Synonyms=BCORE-Q2-Z1;
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Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
.M., Cambbell L.A., Darlamiteou A., Henderson N.S.,
J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.
                                    =Q01Z95-3; Sequence=External Synonyms=BCORE-Z2;
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InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00056; Zf-C2H2; 2.
SMART; SM00355; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 2.
PROSITE; PS0007; BTB; 1.
PROSITE; PS0007; BTB; 1.
PROSITE; PS0007; BTB; 1.
Interpretable proceeding to the process of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no resume by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U51585;
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SIMILARITY: Contains 2 C2H2-type zinc fingers.
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS
TO 619 AND 656 TO 694 DUE TO FRAMESHIFTS.
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ISOId=Q01295-5; Sequence=External;
DEVELOPMENTAL STAGE: ACCUMULATES TO A HIGH LEVEL AT THE BEGINNING
OF THE ECDYSONE RESPONSE, DURING THE METAMORPHOSIS OF IMAGINAL
DISKS IN PUFF STAGE 1, AND ABRUPTLY DISAPPEARS AFTER SEVERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION: INDUCED AS A PRIMARY RESPONSE TO 20-HYDROXYECDYSONE THIRD INSTAR LARVAL IMAGINAL DISKS.
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AE003421; AAF45647.1;
                                                                                                                                                                                                                                    37
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 PANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIASAVT
                                                                         TATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAAT
                                                                                                                 GSSTLFSRQGAGSPPP--TAVPSLPSH-----INNQLLKRMA---MMHRSSA
                                                                                                                                                   SENNQTSHDSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAA
                                                                                                                                                                                          LKTAEVLRVSGLTQQQAEDTHSHLAQIQNLANSGGRTPLNTHTQSLPHPHHGS--LHDDG
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92305 MW;
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                                                               TAMB DROME STANDARD; PRT; 883 AA.

P11536; Q9VVI7;

101-OCT-1989 (Rel. 12, Created)

P101-OCT-1989 (Rel. 12, Last sequence update)

P115-SEP-2003 (Rel. 42, Last annotation update)

E Ecdysone-induced protein 74EF isoform B (ETS-related)

E Ecdysone Fr4 OR CG6285.

DESP04EF OR E74 OR CG6285.

DESP04EF OR E74 OR CG6285.

C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pt.

C Eukaryota; Endopterygota; Diptera; Brachycera; Muscomo.

C Neoptera; Endopterygota; Diptera; Brachycera; Muscomo.

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                        DROME
SEQUENCE FROM N.A. MEDLINE=89315191;
                                                 [_TaxID=7227
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                                                                                                                                                                                                                                                                                                                                                                                                     GPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASGAGGRGGGAGGPGGSLLSSVRAQDVAQANRLLLPLPLNACHRCDVCGKL-LSTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISG-----DVKSVRACATPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAG-IGAMPKLDETQTVGDFIKGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGD-
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 PubMed=2501755;
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                                                                                                                                                                     (ETS-related protein E74B)
                                                                                             Muscomorpha;
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Davies P., Deviller P., Bolson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K. J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Durbin K. J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Laiz R., Houck J., Laiz R., Houck J., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Kalmal B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nelson D.R., Nelson K.A., Nuskern D.R., Pacleb J.M., Renington K., Saunders R.D.C., Scheeler F., Shah H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., RA Yeng X.H., Zhong F.N., Zhong F.N., Zhou X., Zhu X., Zhu X., Smith H.O., Ra Yeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Ra Yeng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O., Ra Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C., Zhu X., Smith H.O., Ra Cheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O., Ra Cheng X.H., Zhong S., Pan S., Pollard J.C., Zhu X., Smith H.O., Ra Cheng X.H., Zhong S., Pan S., Pollard J.C., Zhu X., Smith H.O., Ra Cheng X.H., Wang Z.
                                                                                                                                                                                                                                                                                                                                                      Nucleic [2]
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"Characterization of a putative transcription factor gene expressed in the 20-OH-ecdysone inducible puff 74EF in Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATI MEDLINE=90199900; PubMed=2107982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Puffs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94038699;
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                                                                                                                                              DEVELOPMENTAL STAGE: In mid increase
                                                                                                                                                                                                   Name=B; Synonyms=E74B;
IsoId=P11536-1; Sequence=Displayed;
Name=A; Synonyms=E74A;
IsoId=P20105-1; Sequence=External;
                                                predominant isoform during puff st
constant in late larvae until the
increase during 86-94 hours of development and represent the predominant isoform during puff stage 1. Levels remain relatively constant in late larvae until the premetamorphic pulse of ecdysone. Transcripts are detected again from puff stages 12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cible gene that encodes two ets-related proteins.";
61:85-99(1990).
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nce 287:2185-2195(2000)
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PCR: the in vivo dynamics of early gene expression during
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8223281;
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                                                                                                                                                              instar larvae salivary glands levels
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PROSITE; PS00345; ETS_D
PROSITE; PS00346; ETS_D
PROSITE; PS50061; ETS_D
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                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S04722; S04722.
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SIMILARITY: BELONGS TO THE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Base; FBgn0000567; Eip74EI
GO:0006914; P:autophagy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and 17-21.
INDUCTION: THE EXPRESSION
                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00178; Ets; 1.
S; PR00454; ETSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X15087; CAA33195.1; -. M37083; AAA28494.1; -. AE003523; AAF49324.1; -.
                                                                                                               201
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M37083; AAA28494.1;
                                                                                                                                                                                 al Similarity
177; Conserv
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                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                              AS---ARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQ
                                                                                                                                    LVAESAAT-ATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNR---ARHIAA
                                                                                         TSPPPAAAAPAEASPPAGAELQE-------
ASDCREFKVLYNHLRQQQHHHSPSSPDKTRSTLDDVSKILWERK---
                      SGDVKSVRACATFTFSGRRAY--SEEDLSRALQDVVANKLDARKSASQHHEQRSILD--N
                                           VKDPVNVEEPGAIVDTESVMARQSPSPVASTKVPESLE---EISNKSPPVQEDEEESESV
                                                                 QQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSP-----NSSI
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; ETS_DOMAIN_2; 1.
; ETS_DOMAIN_3; 1.
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378
415
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437
524
630
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703
711
711
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883
869
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0 ASP/GLU-RICH (ACIDIC).
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                                                                                                                                                                                                                             MW,
                                                                                                                                                                                  117;
                                                                                                                                                                                Score 244.5; Pred. No. 9.6e
17; Mismatches
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ARG/LYS-RICH (BAS:
ETS-DOMAIN.
POLY-SER.
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                                                                                         -DGQQAKTQEDPTMKDQDMLEKTRQE
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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A.,
                                                                                         SEQUENCE FROM N.A.

MEDLINE=96269413; PubMed=8682312;

Nambu J.R., Chen W., Hu S., Crews S.T.;

"The Drosophila melanogaster similar bHLH-PAS gene related to human hypoxia-inducible factor 1 alpha a single-minded.";
                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                             Similar protein.
SIMA OR CG7951.
                                                  SEQUENCE FROM
                                                                                                                                                                                      NCBI_TaxID=7227;
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                                                  N.A.
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       Evans C.A., Gocayne J.D.,
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50112; PAS; 2.

Pfam; PF00785; PAC; 1. Pfam; PF00989; PAS; 2.

InterPro; IPR001610; PAC. InterPro; IPR000014; PAS_domain. NyBase; FBgn0015542; sima. InterPro; IPR001092; HLH_basic.

JC4851; JC485

Repeat; DNA-binding; Nuclear protein; Transcription Activator; Coiled coil.
DNA_BIND 72 85 BASIC DOMAIN.

BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF

(BY SIMILARITY)

regulation;

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davan R.D., Dew I., Dietz S.M.,
RA Chosin D., Delther A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.I.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler B.C., Stden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler B.C., Stden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler B.C., Stden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler B.C., Stden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler B.C., Shong F.N., Zhong F.N., Weinstock G.M., Weissenbach J.,
RA Yell S.N., Noodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Syler B.M., Roman S., Pollard J.S., Zhao Q., Zheng L.,
RA Kender B.M., Roman S., Pollard J.C., Shou M., Shou S., Zhu X., Smith H.O.,
RA Sheng X.H., Zho
                                                                                                                                                                                                                                                                                                                                                                                                                           currences requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXCRESSED IN THE EMBRYO.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS. HIGHEST TO HIF-1, ALPHA.
-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003772; AAF57008.2;
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              PNSLTQEDDESFEAFAMRAPYIPIDDDMPLLTETDLMWCPPEDLQTMVPKEIDAIQQQLQ
                                            PNS----SISGDVKSVRACATPTPSGRRAYSEEDL----SRALQDVVANKLDARKSASQ
                                                                            QQQQQHHPQHHDNSNSSSNIDPLFNYREESNDTSCSQHL-HSPSITSKSPEDSSLPSLCS
                                                                                                                                          TPNSTATASNPSHQQQ-----
                                                                                                                                                                        SARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQ
                                                                                                                                                                                                      TCLLPEDINSLDSTTCSTTASGOHYQSPSSSSTSAP----SNTSSSNNSYANSP--LSPL
                                                                                                                                                                                                                                                                      PQQPAQDMSKGFCSLFADDGRGLTMLKEEPDDLSHHLASTNCIQLDEMTPFSDMLVGLMG
                                                                                                                                                                                                                                                                                     DSSRTPTPGATSTPSP----------
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S -> L (IN REF. 1).
A -> V (IN REF. 1).
T -> I (IN REF. 1).
T -> I (IN REF. 1).
C -> QOQU (IN REF. 1).
Q -> QO (IN REF. 1).
Q -> QO (IN REF. 1).
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Pred. No. 0.00021;
7; Mismatches 433
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                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                     PROS_DROME STANDARD; PRT; 1403 AA P.29617; Q95SP0; Q9UGA2; Q9VGPB; P.29617; Q95SP0; Created) 01-FEB-1996 (Rel. 33, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                         Protein prospero. PROS OR CG17228.
SEQUENCE FROM N.A
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RA Abrill J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Balwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dudson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Brothin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W. RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C., Jasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Land Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Alali M., Kalain G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Smith T., RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T., RA Shue E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Walls S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Theng Y., Pan S., Pollard J., Yang S., Yao Q.A., Yeh R.-E., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zheng L., Glimbas S.M., Wusers E.W., Rubin G.M., Venter J.C., Theng L., Shith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINBE20196006; PUDMEGILIVILLE,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ganglion Brochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93083413; PubMed=1842358; Chu-Lagraff Q., Wright D.M., McNeil L.K., Doe C.Q., "The prospero gene encodes a divergent homeodomain controls neuronal identity in Drosophila."; Development Suppl. 2:79-85(1991)
REVISIONS, AND AL'
STRAIN=Berkeley;
MEDLINE=22426069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=20503846; PubMed=11051550;
MEDILINE=20503846; PubMed=11051550;
Xu C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.;
"Overlapping activators and repressors delimit transcriptional response to receptor tyrosine kinase signals in the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92171948;
Matsuzaki F., Koiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein that is involv Drosophila."; Cell 67:941-953(1991).
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"Drospero is expressed
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Vaessin H., Grell
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zumi K., Hama C.,
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E., Wolff E., B
PubMed=12537572;
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PDB; 1MIJ; 04-DEC-02. F1yBase; FBgn0004595; pros. GO; GO:0045179; C:apical cortex; GO; GO:0045180; C:basal cortex; GO; GO:0005634; C:nucleus; IEP.

cortex;

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ALT_FRAME

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EMBL; M81389; AAA28841.1; -.
EMBL; D10609; BAA01464.1; -.
EMBL; Z11743; CAA77802.1; -.
EMBL; AF190403; AAF05703.1; -.
EMBL; AE003691; AAF954628.2; -.
EMBL; AE003691; AAM13500.1; -.
EMBL; AE003691; AAM13501.1; -.
EMBL; AE003691; AAM13501.1; -.
EMBL; AY060680; AAL28228.1; ALT
PIR; S24548; S24548.
PDB; IMIJ; 04 DEC-02.
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Wan K.H.,
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY TO C.EI MEDLINE=94212446;
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Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trends Biochem.
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Champe M., Chavez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A STRAIN=Berkeley; TISSUE=Head;
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                                                                                                                                                                                                                                                                                                                                                                                                 ISOId=P29617-4; Sequence=VSP 002308;
TISSUE SPECIFICITY: NEURONAL PRECURSORS. EXPRESSED DEVELOPING CNS, LEWS-SECRETING CONE CELLS OF THE EY DEVELOPMENTAL STAGE: EXPRESSED IN NEURONAL PRECURSO FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nds Biochem. Sci. 19:70-71(1994).

FUNCTION: Required for proper neuronal differentiation all neurons and their precursors in central and periphe systems, axonal outgrowth and pathfinding. Not required specification of neuronal identity. May regulate transc
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS
CAUTION: Ref. 7 seque
                                                                                                                                                                                                                                                                                                                                                       frameshift in position 1122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding to DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eton M., Brokstein P., Hong L., Agbayani A., Carlson J.W. e M., Chavez C., Dorsett V., Farfan D., Frise E., George lez M., Guarin H., Li P.W., Liao G., Miranda A., Mungall J., Pacleb J.M., Paragas V., Park S., Phouanenavong S., H., Yu C., Lewis S.E., Rubin G.M., Celniker S.E.; tted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nme=C; Synonyms=L;
IsoId=P29617-1; S
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                                                                                                                                                                                                                               s requires a license agreement (S an email to license@isb-sib.ch).
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5; PubMed=7909177;
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ci. 19:70-71(1994)
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Developmental protein protein
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                               358
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If protein; Transcription regulation; DNA-binding; Homeobox; pomental protein; Alternative splicing; 3D-structure.
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                             QDDAQDEEDAAPT-GQRSESRAPEEPQLPTKK
                                                                          QDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAE-----
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GLN-RICH.
ASN-RICH.
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POLY-ASP.
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GLN-RICH.
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NUCLEAR LOCALIZATION
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CYA1_DROME STANDARD; PRT; 2248 AA. P32870; Created) 01-OCT-1993 (Rel. 27, Created) 01-OCT-1993 (Rel. 27, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Ca(2+)/calmodulin-responsive adenylate cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00211; guanylate_cyc; SMART; SM00044; CYCc; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0007591; P:molting cycle (sensu Insecta); IGI.
GO; GO:0008355; P:olfactory learning; NAS.
GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.
InterPro; IPR001054; G_cyclase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN=Canton-S; TISSUE=Head;
MEDLINE=92154664; PubMed=1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Base; FBgn0003301; rut.
GO:0019933; P:cAMP-mediated signaling; NAS
GO:0007625; P:grooming behavior; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: Binds 2 magnesium ions per subunit (By simila ENZYME REGULATION: Activated by calcium/calmodulin and SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: MUSHROOM BODIES OF THE FLY BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: Binds 2 magnesium ions per subunit
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 QESTRNGNASDCSSNN-GGSSSTCAKKESISAKIIGCIDLSR----EGASENTTSOGHH
                                GTAAGAAIATKSPFERELQRLLNESSRARCLATATTTAGAISTTDQTASNGSRELS----
                                                                   GYSAGNSLLTSS--SSSIQKMM----
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N-LINKED (GLCNAC. ..) (POTENTIAL)
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MAGNESIUM 2 (VIA CARBONYL OXYGEN)
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Ş	737	SAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLV 776	
ያ	1814	SSHHKTEQQQNMDHEHLAGGKLLGSNSFMIAKHPVGLEAIKEITRNKNPSESSQMQTSDT 1873	ω
γ	777	EAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKER-HLMRPRKREPK-PQP 824	
· ·	1874	ESCEILHENRNOMHVLAMLEMHTAKELNGSHAHHGQHHHQQPQRTHRQRPRSKELQYSHE 1933	ω
γ	825	DLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNONNQAAAAAAAAAAAAAAAATPNGLKLP 884	
· 8	1934	SLDGLDG 1948	æ
Ŋ	885	LFEAGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVY 944	
ъ	1949	RNQRYHHHHHHQQRQQQQRYNHVQEQEERDDTEDNLA 1986	on
Ŋ	945	DGIIRKTLQASEGNGSAAGNGSNGSNGHGHGHGHGHALLDQLLVKKTP 994	•
Ъ	1987	DEEFEDDEVGRDVRQKRLQKSE 2008	ω
Ą	995	LPFTNHRNNDYAATCSSASGESVKRSGSPMGNYADIKRERLSADSGGSSDEEHSASHINN 1054	44
ğ	2009	LNHKRSEVATEAGNHHDDEVEEEDDDDDEEDHR 2042	2
Ŋ	1055	NNSDLAHNKNKSGGGGGGGGGGUNGNGRSSRMTSRDDSETDASSFKSGENGGQQNHKMM 1114	42
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₽ B	2081	DSNPLESOSEWSDDDCREEATGGAESTGYITDEPGLENISLLNE 2124	
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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 107007

TO: Minh-Tam Davis

Location: cm1/8a01/8e12

Art Unit: 1642

Wednesday, October 29, 2003

Case Serial Number: 10/016768

From: Susan Hanley

Location: Biotech-Chem Library

CM1 6B05

Phone: 305-4053

susan.hanley@uspto.gov

Search Notes

RUSH

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	л . Б	ID	Description
N	4839	80.2	1221	ហ	Q24079	
ω	707.5	11.7	1598	v	Q95YM8	
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7	314.5	5.2	5322	Ç,	Q9VPL9	
œ	311.5	5.2	2112	v	Q9VEL9	Ψ
9	310.5	5.1	2038	տ	Q9W3L3	ω
10	309.5	5.1	2151	ū	Q9Y1L3	
11	308.5	5.1	1103	v	Q9VY72	.~
12	305	5.1	1444	v	Q9VTN2	
13	305	5.1	1514	ຫ	Q8SY55	
14	304	5.0	1249	ഗ	QBINC6	Q8inc6 drosophila
15	302	5.0	1140	ഗ	Q8T1T0	_
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5	4.6	4.6	4.6	4.6	6	6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	8	4.9	4.9	4.9	4.9	4.9
1338	2283	1329	1785	67	18	2150	1186	929	929	1741	2302	2280	929	1768	1741	1416	1180	1721	1409	939	1404	1880	2310	4001	3381	1556	1408	1162
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Q8mn23	Q8vq99	Q9w283	Q8i5z0	Q9vqi9	Q9vra6		Q9ved3	Q9ngw5	Q9nbl3	046095				Q24153	Q9w517	Q9vym1			Q9vx60	Q9nhq0	Q8iry3	Q8mp27	Q9gra9	Q8wrq7	Q9kx33	Q9vx23	Q24341	Q9w3q5
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ALIGNMENTS

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Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., G Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., H Hostin D., Houston K.A., Howland T.J., Wei MH., Ibeg Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D	RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dun RA Dodson K., Doup L.E., Downes M., Dudan-Rocha S., Dunkov B.C., Dun	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Che Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch G. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bol	[1] SEQUENCE FROM N.A. STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goc. Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., George R.A., Lewis S.E., Richards S., Ashburner M., H	CG18389 protein. EIP93F OR CG18389. Drosophila melanogaster (Fruit fl Eukaryota; Metazoa; Arthropoda; H Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Droso NCBI_TaxID=7227;	RESULT 1 Q9VD60 ID Q9VD60 PRELIMINARY; PRT; 1165 AA. AC Q9VD60; PRELIMINARY; PRT; 1165 AA. DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAR-2002 (TrEMBLrel. 22, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
chmann K., Chum K.	er P., s P., s P., etz S.M., B.C., Dunn P.,	hen L.X., Pfeiffer B.D., , Miklos G.L.G., C., Baldwin D., , Beasley E.M., olshakov S.,	ocayne J.D., , Galle R.F., Henderson S.N.,	gota; a;	

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A Carlson M.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Ferriera S., Frise E., Galle R.F., Gary N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Kruse D., Li P., Mattei B., Moshrefi A.,

MCINTOSH T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

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                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ EMBL; AE003737; AAF55940.3; -. FlyBase; FBgn0013948; E1993F. SEQUENCE 1165 AA; 123976 MW; A2556014070BE
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01-NOV-1996 (TrEMBLrel. 01)
01-OCT-2002 (TrEMBLrel. 22)
Ecdysone-regulated (E93)
EIP93F OR E93 OR CG18389
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Woodard C.T., Baehrecke E.H., Thummel C.S.;

"A molecular mechanism for the stage specificity
prepupal genetic response to ecdysone.";

Cell 79:607-615(1994).

EMBL; U25686; AAA83228.1; -.

FlyBase; FBgn0013948; Eip93F.

FlyBase; FBgn0013948; Eip93F.
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Baehrecke E.H., Thummel C.S.;
Bare Drosophila E93 gene from the 93F early puff
tissue-specific regulation by 20-hydroxyecdysone.
Dev. Biol. 171:85-97(1995).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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Mblk-1 protein.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoneoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apidae; Apis.

NCBL_TaxID=7460;
[1]
                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Takeuchi H., Kage E., Sawata M., Kamikouchi A., Ohashi K.,

Fujiyuki T., Kunieda T., Sekimizu K., Natori S., Kubo T.;

"Identification of a novel gene, Mblk-1, that encodes a put

transcription factor expressed preferentially in the large-
cells of the honey bee brain.";

Insect Mol. Biol. 10:487-494 (2001).

EMBL; AB047034; BAB64310.1; -.

SEQUENCE 1598 AA; 174929 MW; E5475BDD3ACBIEEF CRC64;
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Db 899INNQSVPLIPNTVNNIPNAPPPPVYEPVDK-QYKTIKHPLTRVSSEPSI 946	334 EULSKALQUVVANKLUAKKSASQHEQXKSILUNINNININININININININININININININININI	807 QDESITPRELSRRNSSSGLILNSPSRNNNINNINNNNGSTKKGTTKLPTLK		Qy 158 TSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASRATPAAATPANSLE 217	SHUSSKIPIPGAISIPSPPPEPIDWKPSAKCNFCVNGKDDIVNAQGKDVAESAAIAISS :::: NNNNNNN	38 EEQQPIAIAGSEDEPSQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQT	Best Local Similarity 18.3%; Pred. No. 2.8e-10; Matches 206; Conservative 172; Mismatches 393; Indels 356; Gaps 35;	KW Hypothetical protein. SQ SEQUENCE 2472 AA; 278497 MW; 30CCF7157D4008A7 CRC64;	RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; RT "Sequence and Analysis of Chromosome 2 of Dictyostellum."; RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; AC115593; AAL92295.1;	RP SEQUENCE FROM N.A. RC STRAIN-AX4; RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., RA Lehmann R., Baumdart C., Parra G., April J.F., Guigo R., Kumpf K.,	.ctyc	- 500	4 FI	03 ISRAGSRDEDS	1354 YRGPSASGGRPVPERPERVPTVDLSPSPSDRGRNDDGSDRLTSPPTPLS		Db 1237 REREGVGAGIAETSAGTSNSRGAAQMSKVPRDVSEGIYDGSGANGSFLDNLIRSSLETGI 1296	Db 1181 VPTILPEQYFATSRIRGLQEQQRNAAMVQQQQQQQQQQQQQQQQQQQQQQQQHQA 1236 QY 955 SEGNGSAAGNGSNGSNGNGHGHGHGHGHGHGHALLDQLLVKKTPL 995

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aLIDQLCRNSRRTPVPRLAQDS--SEDES 1353
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)ÓEDR 1438
                                         QNHK 1112
                                                                                     SRNDDG------SDRLTSPPTPLS 1402
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      Query Match
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Q8SSW3;
01-JUN-2002
01-JUN-2002
01-OCT-2002
                                                                Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K. Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Erythrocyte membrane protein PFEMP3.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                 SEQUENCE
                                                                                                                                                                                               STRAIN=AX4;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID=44689;
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RX MEDLINE-2019(006); PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Dan, Ketchum K.A.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Menkulov G., Milshina N.V., Mobarry C., Morris J., Welson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Shopkern D.R., Shen H.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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Q9VPL6;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                      SSAAQLQKQQQQQQQQQQQQHSMPGPQNLTGEEPVPVINKQTGKRLGGNKAPQLKRLM 123
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                                                                                SSL-GYKKPSI----SVAKIIGGTDTSRFGA
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Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Pandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Daybayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brosstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Podler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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InterPro; IPR000330; SNF2_N.
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
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Celniker S.E., Adams M.D.,
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X., Smith H.O.,
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1.D., CEIL. ted (MAR-2000) S.E., ç the Gibbs R.A., Rubin G.M., e EMBL/GenBank/DDBJ datal databases

(SEP-2002) င the EMBL/GenBank/DDBJ databases

Modifiers

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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL, AE203590; AAFF31527.3; -EMBL; AF215703; AAF43004.1; -HSSP; P23197; 1AP0. FlyBase; FBgn0001309; kis. InterPro; IPR000953; Chromo. InterPro; IPR001410; DEAD.

Pfam; PF00271; helicase C Pfam; PF00176; SNF2 N; 1 SMART; SM00298; CHROMO; 2

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SEQUENCE 5322 AA; 573615 MW;
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NPYSLGSSGLGSAYDQ--LAQQYNLLNGATSSASNTSSTQSKSHQSQSKSSQSRNTTASA
                                 RP----KRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPR
                                                                                                                                  GNLAGMDTQSLAALMAAAGPTLGGLTGASGGAGSGKSQAQSQSSATSSSSSASKKKQQQQ
                                                                                                                                                                  SSL-GYKKPSI-----SVAKIIGGTDTSRFGA-----SPNLLSQQHHSAHHLTHQQQ
                                                                                                                                                                                                     FDPKNPLAAFDPKNPLLSMSFGGMPGM--GNI----PGLGNLNNMNLFASLAGMGGL
                                                                                                                                                                                                                                                                     HTQQQSSAAQSQAGGNSGSSKKNSRQQTAASAALDQAALQFGSLAGLNPSLLANLPGLGA
                                                                                                                                                                                                                                                                                                     NSNHSSNSHRN--GSN------RSPHSASPMLAAAVAQGGYSAG-------
                                                                                                                                                                                                                                                                                                                                                                       ---SEDPILKI-PSF--KVSGPASSSSLSPGGLVGGH-----HHPLNNNNSLSISN
                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLQQQQHQQHHQQHHQQQQQQQHVAAYRHRLPKSETP----ETNSSLDPNDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMGGLSSKDSLNALLAQTMATDPQTFLKQQQKMMQFLPPAQRKAYENMLAEMEQAM-KIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANLQSSSNQQSNQKPFTITVTTVPGKSKSGSSNSGSGTGGSSSASGGGAGGSGLSALQNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSG------NRARHIA- 199
                                                                                                                                                                                                                                    -----NSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGS
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20.4%; Pred. No. 1.2
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gebart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gebart W.M., Glasser K.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Molson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VEL9; PRELIMINARY;
Q9VEL9;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG4090 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BERKELEY;
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Last annotation updat
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                                                                                                                                    K.A.,
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RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RR EMBL, ABO03716; AAF55402.1; -.
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Best Local S
Matches 225
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SMART; SM00494; ChEBD2; 11.
PROSITE; PS00022; EGF 1; 1.
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InterPro; IPR002557; Chitin bi
InterPro; IPR006209; EGF_like.
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2112 AA; 219547 MW;
                                                                                                                                                         GGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKK
                                                                                                                                                                                                            QGSSS
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                                                                          PSISVAKIIGGTDTSRFGASPNLLSQQHHSAHH---LTHQQQQQQLSAQEALGKGTRPKR
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18.9%;
                                   -SSSNQGSSSNQGSSNQSSNQGSTSSSSNQSSSSSNNNSTSTQTKPSN
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Pred. No. 5.0
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Q9W3L3
RX MEDLINE=20196006; PubMed=10731132;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Ceorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G.; Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G.; Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G.; Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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01-OCT-2002
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pto
Neoptera; Endopterygota; Diptera; Brachycera; Muscomos
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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140 NAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSSNNNSSGNRARHIA 199	Query Match 5.1%; Score 310.5; DB 5; Length 2038; Best Local Similarity 20.8%; Pred. No. 6.1e-09; Matches 234; Conservative 125; Mismatches 331; Indels 437; Gaps 48;	PROSITE; PS50014; BROMODOMAIN 2; 2. PROSITE; PS00583; PFKB_KINASES 1; 1. SEQUENCE 2038 AA; 205346 MW; DC4A1A7B1266191E CRC64;	Z 1	PRINTS; PRO0303; BROWODOWAIN. PRINTS; PRO0303; BROWODOWAIN.	Pro; IPR001487; Bromodo Pro; IPR002173; PfkB.	FBgn0004656 IPR000104;	312.3;		(MAR-2000) to the EMBL/GenBank/DDBJ datak	SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.; "Annotation of Drosophila melanogaster genome":	Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,	Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,	[3] SEQUENCE FROM N.A.	"Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;	Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,	Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,	:	Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,	Gocayne J.D., Amanatides P.G., Brandon I n H., Baldwin D., Banzon J., Beeson K.Y	SEQUENCE FROM N.A. Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,	Science 287:2185-2195(2000).	"The genome sequence of Drosophila melanogaster.";	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	ָאֲ נְ . אֱ	Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	Shen H	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Waldrip W.R., Scott M.P., Kennison J.A., Tamkun J.W.;
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Development 126:1175-1187(1999).
EMBL; AF113847; AAD37500.1; -.
FlyBase; FBgn0001309; kis.
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CG32611 OR CG11075 OR CG11082.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
SEQUENCE FROM N.A. STRAIN=Berkeley; MEDLINE=20196006;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00225; BTB; 1.

SMART; SM00355; ZnF_C2H; 4.

PROSITE; PSS0097; BTB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.

PROSITE; PS0157; ZINC_FINGER_C2H2_7; 4.

Metal-binding; Nuclear protein; Zinc; Zinc-finger.

Metal-binding; Nuclear protein; EB586FD5683C9BOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00308; ANTIFREEZEI. PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00651; BTB; 1. Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003494; AAF48333.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR
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                                                                                                                                                                       QESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGAS
                                                                                                                                                                                                                                                            HSASPMLAAAVAQGG----YSAGNSLL-----TSSSSSIQKMMASNIQRQINEQSG
                                                                                                                                                                                                                                                                                                                                                                                            HQN------LQRLHHTHHHAQH--QHSQHHHPHSQHHHTPHHQQHHTHS--DDEDAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGGHHHQRQVM------DDRLEQDVDEEDLDDDVVVVGPATAMARGIAQRL--A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPS 326
EAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANKL
                                          PVQSVPLSLKKEIDCSEDDNSSH--SRHMQQRSASAGGGLG-GDLDYRASHESETSES--
                                                                                                                                                                                                                                                                                                                                                 DPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSNSHRNGSNRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                QENSNGNASLLLQQQQQQQQHQQHHQQQHQQQQQQQHVAAYRHRLPKSETPETNSSLDPNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHTNSSSNSNNNNNNNNNSSSNNNNNTSSGKTSASSNGGTASSGGTADSVVAVDDDDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENEETKLRGRDEDDDDEDEEEDTPMPLDLYQRPNVEPKSAAAATAAQQGGSNSLSGSSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRSSRMHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAATSSSSSVTSAAAAAA----AAASASGVAHSEEATSSSSSTGGQKREASDRSSPTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAAAGSSN----TTTTTAATTTATCATAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATQAATATATATAAA-------ATSTSTSATSAAATAAATAATSASTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AESAATATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLNLLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                    -MGSGGAGGGGGVDLSTGSTLIPSPLITLPSSSAAAAAAAAAAAAAASQRSTPAMSA
                                                                                                                                 -ASDLSIGGCGG-----RPASRSSRDGGGNDGGRGGASSSSLLSPGTVANLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NDDAEAEVDSNASTPVY-----PAEFARAQLRKLSHLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1%;
                                                                                                                                                                                                                                                                                                       -AKSEILDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                  SQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - ADKVDVAEDREQEQNOADELLSEELLGRNLKDEEDDDVDELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.5; DB 5
Pred. No. 3.6e-09;
80; Mismatches 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         -DYDDEMDLEDDDEADNSSNDLGLNMK-
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243

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681 543 459 514 413 461 353 421 293

836

776 650 <u>ن</u>

1103; 373;

Indels Length CRC64;

Gaps

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PRA HOD RA HOD RA HAD R
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boxendale J., Bayraktaroglu L., Beasley E.M.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Gawley S., Dahlke C., Davreport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrae C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., Kraft C., Kranison J.A., Ketchum K.A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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Q9VTN2;
01-MAY-2000
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG6004 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNGSAAGNGSNGSNGNGHGHGHGHGHALLD-QLLVKKTPLPFTNHRNNDYAATCSSASGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASE
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22,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1444
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

A McIntosh T.C., Moy M., Murphy B., Patel S., Pfeiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

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"Sequencing of Drosophila melanogaster genome.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Friee E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
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Submitted (MAR-2000) to the EMBL/Genmant/non---
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Pfam; PF01607; CBM_14; 3.
SMART; SM00494; ChtBD2; 3
SEQUENCE 1444 AA; 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0036203; CG6004.
InterPro; IPR002557; Chitin_bind_PerA.
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                                 HHISSSSSSNNNSSGNRARHIA----AASARATPAAATPANSLEL-----YKLLTQRAAKM
                                                                        -SWESHISTDSSIGSKVESILIEALYSLIQES-SSSSSSPVSNEPSTGATDDSSSTESLP
                                                                                                            IDWRPSAKCNFCVNGRL--LTVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLP
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Pred. No. 8e-09
93; Mismatches
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EMBL/GenBank/DDBJ
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                                                                GHHT----TSILHEKLAQIKAEQVDQAD 1163
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                      KYTTEGNKAETSTLKSPTGTTPGHQEDRTD
                                                                                                                                                                                              {\tt SSTPGNDDDSGNSGSENGNSSTSGSPCTTDNPSDPESSSSTPGNDDDSGNSGSESGITST}
                                                                                                                                                                                                                                      KNKSGGGGGGGGGQTNGNGRSSRMTSRDDSETDASSFK-----
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLEQQHNGSQLLEEEDSENNQTSHD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFQFINSAVGIEPLSQDNLADKDKKDIISSSSDSSPTEDATYSSTQVSST----
                                                                                                                                                                                                                                                                                                  ---STEATNESSSTESSODSTTQESSSSTEGPLSTESSTEATNESSSTESSOD-----
                                                                                                                                                                                                                                                                                                                                                                                          SSTESQPDSTTQESSSSTEGPLSTESSTAVTDQSSSTESSQDSTTQESSSSTEGPLSTES
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  LLLQQQQHQQHHQQHHQQQQQQQHVAAYRHRLPKSETPETNSSLDPND---
                                        STEDPLSTESSTEATNESSSTESSOD----STTOESSSSTEGPLS-TESSTEGSNESSS
                                                                                                                               TEATNESSSTESSODSTTQESSSSTESP-LSTEP---STEANESSSTESSODSTTQESSS
                                                                                                                                                                                                                                                                                                                               PSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                  TSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQIASAVTPTTSEVSAAAISPALKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSTQESSSSESPVSFELSTEATNESSSSESLPNSSTQDSSSSTETSFQTESTTDATDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHISSSSSSNNNSSGNRARHIA---AASARATPAAATPANSLEL----YKLLTQRAAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDWRPSAKCNFCVNGRL--LIVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLP 177
                                                                                     ----LMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLNLLSASQENSNGNAS 523
                                                                                                                                                                          ARAQLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHT- 468
                                                                                                                                                                                                                                                        ARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SWESHISTDSSIGSKVESLLIEALYSLIQES-SSSSESPVSNEPSTGATDDSSSTESLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 305; DB 5; L
ilarity 18.1%; Pred. No. 8.5e-09;
Conservative 193; Mismatches 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                    STTQESSSSTEGPL--STESSTEATNESSSTESSQDSTTQESSSSSEGPLSTESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157140 MW; 1FFC4B0664105AD5 CRC64;
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CG3992-PB.
SEQUENCE FROM N.A.

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goca Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., George R.A., Lewis S.E., Richards S., Ashburner M., He Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Che
                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Archropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHSSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKWASNIQRQINEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAPYTTONPASQEPSPSAPENPGDSGNSSSESPPEGATPCTPNAPKKSTTSSYTAHPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNKSGGGGGGGGNGQTNGNGRSSRMTSRDDSETDASSFK-----SGENG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGHALLDQLLVKKTPLPFTNHRNNDYAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSTEANESSSTESSODSTTQESSSSTEGPLSTESSTEASNESSSTESSODST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSTTQESSSSTESPLSTEPSTEANESSSTESSQDSTTQESSSSTEGPLSTEPSTEANES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CSSASGESVKRSGSPMGNYADIKRERLSADSGGSSDEEHSASH----INNNNSDLAHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTNATNAYGLDFNRITEAMR----
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Last annotation updat
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                                                             Gocayne J.
                                                                                                                                                                                                                                                                                Pterygota;
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                                    RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C.R., Babdwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beseson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibeyama C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeyama C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Agier E., Siden Kianos I., Simpson M., Strong R., Pacleb J.M.,
RA Agier E., Siden Kianos I., Simpson M., Strong R., Pacleb J.M.,
RA Spier E., Siden Kianos I., Simpson M., Strong R., Pacleb J.M.,
RA Williams S.M., Moy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L.,
RA Williams S.M., Woodaget, Worler R., Venter E., Wang A.H., Wang X.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Weits G. W., Weits C.,
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Evans C.A.,
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Tupy J.L., Bergman C.,
Clamp M., Drysdale R.,
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                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbel Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D. Tupy J.L., Bergman G., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E "Annocation of Drosophila melanogaster genome.";
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Misra S., Crosby M.
Hradecky P., Huang
                                 Submitted (SEP-2002)
EMBL; AE003711; AAN1
SEQUENCE 1249 AA;
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Submitted
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Evans C.A., Gocayne J.D., Amenatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRARHIAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLIN
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                                                                                                                                                    HGGSKLSNALKNONNOAAAAAAAAAAAAAATPNGLKLPLFEAGP-QALSFOPNMFWPOT
                                                                                                                                                                                                                                                                                                                           LTHQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLASQQQQQQ-----QQIAS--AVTPTTSEVSAAAISPALKDTP------SPSVDAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKAQNDASESVK-----TKVISYHQSEDQQQQQQQQQQQQTEQQQQFLSQQLISHHQQEQ
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GSNGSNGNGHGHGH-GHGHALLDQLL----
                                      ----YQQQQLLMADQHSSAASSPHSM-----
                                                                            NATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGN
                                                                                                                    NAIMESGSLVTNCHN----VGVVLDSSQMDVNDDMKPQLDLKPYNSYSSQPQQQLPQ-
                                                                                                                                                                                                  EPVCNACGLYYKL-HSVPRPLTMKKDTIQKRKRKPK-----GTKSEKSKSKSKNAL
                                                                                                                                                                                                                         EMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGP
                                                                                                                                                                                                                                                                                     LCNACGLYMKMNGMNRPLIKOPRRLSASKRAGLSCSNCHTTHTSLWRRN-----PAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRGQNDTWFDPLSYATSSSGQAQLGVGVGAGVVSNV-----IRNGRAISAANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSAGN-----SLLTSSSSSIQ-----KMMASNIQRQINEQSGQESLRNGNVSDCSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAAATAAVNGHNS-SLEDGYGSPRSSHSGGGGGTLPAFQRIAYPNSGSVERYAPIT--N
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9%; Pred. No. 7.6e-09;
176; Mismatches 470; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                         -YKKPSISVAKII------GGTDTSRFGASPNLLSQQHHSAHH
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--VKKTPLPFTNHRNNDYAATC---
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EMBL; AC116102; AAL93607.1; -.

InterPro; IPR000198; RhoGAP.
Pfam; PF00620; RhoGAP; 1.

SMART; SM00324; RhoGAP; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 124.5 kDa protein.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QST1TO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 1140 AA; 124451 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSTSLSPSAMSHQHQTHPHQQQQQQLCSGLDMSPNSNYQMSPLNMQQHQQQQ---SCSMQ 988
                                                                                                              AVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGR
                                                                                                                                                          QAFKRVKNINGNNKLKKEIEELTNKTGLNQQYTHSNL--PFNVVES-----DIDNGSSG 198
                                                                                                                                                                                                                                                                                SHIHOHDSDSNSSASLPHHISSSSSSSNNNSSGNRARHIAAASARATPA----AATPANSL 216
                                                                                                                                                                                                                                                                                                                             --PSTTSTSS-----
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STEDYTDIPRII---
                                   RAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDS 388
                                                                              GTTSSTGNI-
                                                                                                                                                                                                                                            SPLHNONONONIOLN---SSSGSLNNNEQQQQQQSISQTSSPNTSSPIMGKKKPSRLA 147
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                                                                                                                                                                                                  ELYK------LLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SSASGESVKRSGSPMGNYADIKRERLSADSGGSSDEEHSASHINNNNSDLAHNKNKSGG 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 175; Mismatches 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 302; DB 5;
Pred. No. 8.8e-09;
                                                                                                                                                                                                                                                                                                                             -----YIDSASSSIEETSGYLSKTSSSSSLPS
  KMSVEYLFEKCLLVPGIFR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1140
                                                                              -ISHSKSPSSSSSSSSKKHORKSRFIEPISO 238
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A;Title: The Drosophila pipsqueak gene encodes a nuclear BTB-domain-containing protein A;Reference number: 222972; MUID:96232300; PMID:8674425
A;Accession: T45461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 'MQ',428-1085 <WE2>
A;Cross-references: EMBL:X90986; NID:g1149498; PIDN:CAA62475.1; PID:g1149501
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A;Map position: II
A;Introns: 427/3
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A;Residues: 1-355,'E',357-1005,'H',1007-1020,'Q',1021-1061,'ERS' <HOR>
A;Cross-references: EMBL:U48358; NID:g1203906; PIDN:AAC47153.1; PID:g1203907
A;Experimental source: tissue type ovarian
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A;Accession: S66150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description: required for establishing polarity of the developing egg chamber uperfamily: BRcore-Z protein; POZ domain homology -123/Domain: POZ domain homology -POZ>
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Best Local Similarity
Matches 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 SASGSSGSLAGGQQASQTPSGLQPTPRKSRLKRSKSPDLSSGGGAGSSGGSSSGSTQQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 EQQQQHHQQQQQQQAQEQHQQQQVHAQQQQQQQQQINAALLTQHGVSSGSVSLSGQLLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 EPSQYNHSSKEISQSNPNHCKTENHRLEQQH------NGS-----QLLEE
                                                                                                                                                                  ----QH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQQIASAVTFTTSEVSAAAISPALKDTFSFSVDAFLDLSS------KPSFNSSISGD 313
GVHGQHGGHVTHADIGGATVMEIDPSQIKHEPGMIIT-----PEIVNMMS-----SGHM
                                     -----HRLPKSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHH 604
                                                                                                                                                                                                          RGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKG
                                                                                                                                                                                                                                                 HDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGSDLGEDVD
                                                                                                                                                                                                                                                                                                                                                                            VKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKH
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17.9%; Pred. No. 1.2e-05;
vative 135; Mismatches 398
                                                                                                                                                                                                                                                                                                                                     --HHHTGDESNSNLVQHIKSEVIEAKHLAAQHH----ALSQAQQQHAH
                                                                                                                                                                  -QSQLQQQQQQQQQQHHQQQQQQAAAAAAAA
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search	Db .	γ	В	8	рь	Ş	В	8	망	8	В	Qy	Db	Ş	В	δλ	Вb	δ	Дb	ş
Search completed: October 29, 2003, 12:31:30	1079 KANKOKR 1085	1080 GNGRSSR 1086	1019 QQSPHPGHHPQHMQQDVVTSSSQVVHSQQQQQLQQIYQHHGTPVTASGSSAVSGGTSKRK 1078	1040 GGSSDEEHSASHINNNNSDLAHNKNKSGGGGGGGGGGGGGTN 1079	966 LQQQFPYSPSPHPPTPQHHSTPQHHSSAQQGPPTPQHMQQYVVHMQQQQQQQQ 1018	984 LLDQLLVKKTPLPFTNHRNNDYAATCSSASGESVKRSGSPMGNYADIKRERLSADS 1039	920 SLYGRFKRGKYDVVANTSGVALLNTSGNTTGSIEIIEHSQENSLHM 965	936 AQDMVENVYDGIIRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGHA 983	873 CKREGIELSRSNPTPWSEDAMNEALNSVRVGQMSIN-QAAIHYNLPYS 919	876 ATPNGLKLPLFEAGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKS 935	825 LAAPFNAAPTTWTPEDLERALEAIRAGNTSVQKASAEFGIPTGTLYGR 872	829 LTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAA-AAAAAAAAAAA 875	780 SWNEDALQNALEALRSGQISANKASKAFGIPSSTL-YKIARREGIR 824	769 NYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVG 828	745 SLTKASAIYGIPSTTLWQRAHRMGIETPKKEGGTK 779	709 SISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYR 768	706 GMSGGAGSGSGEKGQFNGPKAWTQDDMNSALDALKNQNM 744	649 GYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKP 708	654 DMYNSDTSEDSMMIANGSPHDQKEPHYTNLDQQHGLGGSVCGPGPGGAGGGG 705	605 HPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQG 648

Search completed: October 29, 2003, 12:31:30
Job time: 64 secs

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RESULT 14
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F90073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315 C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: F90073
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sidues: 1-2271 <KUR>
ssidues: 1-2271 <KUR>
rcross-references: GB:BA000018; PID:g13702612;
pExperimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
  AAI-----SPALKOTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSE :: | ; | | ; | | ; | | ; | | ; | | ; |
                                                                                                                                                                          NSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLELY
                                                            ESDSISESTSTSDSISEAISASESTSISLSESNSTSDSESQSASAFLSESLSESTSESTS
                                                                                                 KLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIASAVTPTTSEVSA
                                                                                                                                                                                                                       ----TSQSGSTSTST-----STSASVRTSESQSTSGSMSASQSDSMSISTSFSDS
                                                                                                                                                                                                                                                     DSSRTPTPGATSTPSPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTS
                                                                                                                                                                                                                                                                                                    ISTSGSLSASDSKSMSVSSSMSTSQSGST--
                                                                                                                                                                                                                                                                                                                                       IAIAGS---EDEPSQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSH
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                                                                                                                                          -DSKSASTAS-SESISQSASTSTSGSVSTSTSLSTSNSERTSTSVSDSTSLSTS
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17.2%; Pred. No. 1.5e-05;
ative 200; Mismatches 506
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K.;
                                                      gene pipsqueak protein A long form - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 23-Sep-200 C;Accession: S66149; S66150; T45461 R;Weber, U.; Siegel, V.; Mlodzik, M. BMBO J. 14, 6247-6257, 1995 BMBO J. 14, 6247-6257, 1995 A;Title: pipsqueak encodes a novel nuclear protein required downstream of A;Reference number: S66148; MUID:96134923; PMID:8557044 A;Accession: S66149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1085 <W
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                                                                                                                                                                                                                                                                                                                                                         TSRDDSETDASSFKSGENGGQQNHKWMDLNGGSSSSSHIKCESEAATGHHSPGHHTT
                                                                                                                                                                                                                                                                                                                                                                                                                                    LSADSGGSSDEEHSASHIN-----NNNSDLAHNKNKSGGGGGGGGNGQTNGNGRSSRM 1087
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y 735 HHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYD	C;Species: Bombyx mori (silkworm) C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997 C;Accession: \$52714 Db	C; A
y 689 NVSDCSSNNGGSSSLGYKKPSISVAKI	RESULT 13 S52714 Db	RESI S52
y 631 NRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQXMMA :	Y 1129 ESEAATGHHSPGHHTTSILHEKLAQIKAEQ 1158 QY :	B 8
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571	1071 GGGGNGQTNGNG-RSSRMTSRDDSETDASSFKSGENGGQQNHKMMDLNG-GSSSSSHIKC 1128	5
y 511 LSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQQQHVAAN	Y 1026 NYADIKRERLSADSGGSSDEEHSASHINNNNSDLAHNKNKSGGGG 1070 Qy	음 ઇ
y 452 QGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIK ; ; ; ; ; ; ; ; ;	969 SNGNGHGHGHGHALLDQLLVKKTPLPFTNHRNNDYAATCSSASGESVKRSGSPMG 1025	
y 404 VYPAEFARAQLRKLSHLSEHNGSDLGEDV 	y 909 AYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNG 968 Qy Qy	B 8
Y 358 HEQRSILDNRLFKMKHHDQEQDHDGDELEDSND	Y 854ALKNQNNQAAAAAAAAAAAAATPNGLKLPLFEAGBQALSFQPNMFWPQTNATN 908 QY	B 8
y 307 NSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQD ::	Y 812 LMRPRKREPKP	유 성
y 247 denlinslasqqqqqqqqqqqiasavtpttsevsaaaispalk 	Y 754 EALGKG-TRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVP-HSTLEYKVKERH 811 Qy	B 8
y 199 AAASARATPAAATPANSLELYKLLTQRAA ; ;;;;; ;;;;;;;;;;;;;;;;;;;;;;;;;;	Y 694 SSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQ 753 QY b 696GSKPTLPMLCPASSSSQVTITPRPRATPSIYSFSEPNIHVPALEIVRLPVNKQ 858 Db	B 8
y 155 SStTSNSHIHQHDSDSNSSASLPHH	Y 658 TSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDC 693 QY	B 성
y 98SHDSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGR 	604HHPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLL 657 QY	
Y 57 HSKEISOSNPNHCKTENHRLEQOHNG	Y 568 DPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGH	B 8
y 5 SYEISLERVAEECMGRROWKHYODKLTCSHLNIEEOOPIAI	Y 510 LLSASQENSNGNASLLLQQQQHQQHHQQHQQQQQQQHVAAYRHRLPKSETPETNSSL 567 QY	B 8
Query Match 4.5%; Score 270.5; DB 2; Best Local Similarity 18.5%; Pred. No. 5.7e-06; Matches 238; Conservative 174; Mismatches 483;	450 ANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLN 509	DP 64
A;Reference number: S52714 A;Accession: S52714 A;Attus: preliminary A;Molecule type: mkNA A;Residues: 1-1217 <gar> A;Cross-references: EMBL:Z48802; NID:g755699; PID:g7557</gar>	491TSTSSSHRKRKKKHSKEPKDANGKRKKLHAEISSQTDGKMKVK 533 398 SNASTPVYPAEFARAQLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNAS 449	04 pp
R;Garel, A.A.; Deleage, G.G.; Prudhomme, J.J. submitted to the EMBL Data Library, March 1995 A;Description: Structure and organisation of the Bombyx	435 ETYAKNIGLKPIEQPLQQSAS-NPDSKYSPNASPMSSCSSSTNGSSSSLGTADASTS 490 343 VVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVD 397	& B

790 903	HHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDR 	8	
734 864	689 NVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQ	0 AG	
688 811	631 NRSPHSASPWLAAAVAQGGYSAGNSLLTSSSSSIQKWMASNIQRQINEQSGQESLRNG	Qy 6	
630 754	571 DASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHPLNNNNSLSISNNSNHSSNSHRNGS	Qy 5 Db 7	
570 709	511 LSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQQHVAAYRHRLPKSETPETNSSLDPN	Qy 51 Db 67	
.510 .	452 QGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGG-IMNEGLLNL	Qy 4 Db 6	
451 619	404 VYPAEFARAQLRKLSHLSEHNGSDLGEDVDRGSPKMGRHPACGNASAN	Qy 4 Ωb · 5	
403 559	358 HEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTP	. op 3	
357 499	307 NSSISGDVKSVRACATFTPSGRRAYSEEDLSRALQDVVANKLDARKSASQH :	Оу 3 Дъ 4	
306 454	247 DFNLINSLASQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSP : : : :	Qу 2 Db 4	
246 428	199 AAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLA	Оу 1 ръ 3	
198 371	155 SSSTSNSHIHOHDSDSNSSASLPHHISSSSSSNNNSSGNRARHI	Oy 1	
154 311	98SHDSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATAT	Qy Db 2	
97 265	57 HSSKEISQSNDHHCKTENHRLEQQHNGSQLLEEEDSENNQT	Qy Db 2	
56 205	5 SYEISLERVAEECMGRROWKHYODKLTCSHLNIEEQQPIAIAGSEDEPSQYN	Оу 1	
45;	Match 4.5%; Score 270.5; DB 2; Length 1217; Local Similarity 18.5%; Pred. No. 5.7e-06; es 238; Conservative 174; Mismatches 483; Indels 389; Gaps	Query Match Best Local Matches 23	
and of the	Dat ure 5271 AR>	submitted to the EMBL A;Description: Struct: A;Reference number: S A;Accession: S52714 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1217 <g a;cross-references:="" e<="" td=""><td></td></g>	

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1449 <HOO>
A;Cross-references: EMBL:X69871
C;Genetics:
A;Gene: FlyBase:f
A;Gross-references: FlyBase:FBgn0000630
A;Cross-references: FlyBase:FBgn0000630
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
F;63-96/Domain: ankyrin repeat homology <AN1>
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ERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAA----
                                                                                                                                                                           CSSNNGGSSSLGYKKPSIS-VAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLS
                                                                                                                                                                                                                                                                                            DIVLOYSNHH---LNNKRNMNNNSNMNNSSSNIAQSSSSSNNNNNSLLNRNKSHSIIGLHS
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                                                                                                AQEALGKGTR PKRGKYRNYDRDSLVEAVKA - - - VQRGEMSVHRAGSYYGVPHSTLEYKVK
                                                                                                                                         ASSNINTSGSIN----NISNIGNMNGGNQSSR
                                                                                                                                                                                                                 SKYESCLKDNYSAKNVNLKNQLLNGGIKSDTYESVCPPEDVAERTKQTHKNSMIRNNLAD
                                                                                                                                                                                                                                                    --AAAVAQGGYSAGNSLLTS-----SSSSIQKMMASNIQRQINEQSGQESLRNGNVSD
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Pred. No. 4.2e-06;
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A;Accession: $16845
A;Accession: $16845
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X56798; NID:g8526; PIDN:CAA40134.1; PID:g8527
A;Cross-references: EMBL:X56798; NID:g8526; PIDN:CAA40134.1; PID:g8527
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
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A;Introns: 55/1; 139/2; 219/3
C;Superfamily: Drosophila suppressor protein of C;Keywords: DNA binding; nucleus; zinc finger F;31-79/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-1365 <BRU>
A;Cross-references: EMBL:X56799; NID:g8528; PID:g8529
A;Cross-references: EMBL:X56799; NID:g8528; PID:g8529
A;Brunk, B.P.; Adler, P.N.
Nucleic Acids Res. 19, 3149, 1991
Nucleic The sequence of the Drosophila regulatory gene
A;Reference number: $16845; MUID:91279476; PMID:2057369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressor two of zeste protein - fruit fly C;Species: Drosophila melanogaster C;Date: 06-Jan-1995 #sequence_revision 06-Ja C;Accession: S14871; S16845 R;Brunk, B.P.; Adler, P.N.
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                                                          AEDFELKTANRKGVGHLPKLKIELNSMKSKLSMPLSA---GPRLEDTSCSSSCSAQQLDL
                                                                                                                                                                         LLTQRAAKMTSMDSMAAQL-------AQFSLLADFNLINSLASQQQQQQ---
                                                                                                                                                                                                                 SEIDSGSPRSKVRCKTPPKVSPSSKNKRLTSSKR
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                                                                                                                                     SL--RSNDMRYSDYAVSKVKSEPEQEQFLLPREREQQPLEANTNIVVSIPPSQLRKSYVD
                                                                                                                                                                                                                                                      SHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLELYK
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ilarity 19.7%;
Conservative 154
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Pred. No. 6.2e-06;
4; Mismatches 398
                                                                                              QQQIASAVTPTTSEVSAAAISPALKDTPSPS-----
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C;Species: Drosophila melanogaster
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
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fntrons: 43/2; 104/3; 164/3; 564/3; 717/3; 825/1; 1001/2; 1121/3; 1204/3;
lperfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
0-83/Domain: ankyrin repeat homology <AN1>
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      SLGGNSSSGGG--
                              SSSSNNNSSGNRARHI AAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQF
                                                            HPPALAGGSGGSGMGLGMGMGMGMGMSMGLGISRKNSDA---LYSOOSRSSSEKLYNGSS
                                                                                             RPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSH1HQHDSDSNSSASLPHH1SS
                                                                                                                           ----OHOOOOOOOOOOHLSSSCNSNSNSSKOTSRSNTIKSKSSSTLSSDVEPFYL
                                                                                                                                                      SNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPT--PGATSTPSPPPEPIDW
                                                                                                                                                                                     RWRQSRSKLSLDKYGKSPINDAAENQQVECLNVLVQHGTSVDYNGKSSSQRHKSQQQLHQ
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19.2%; Pred. No. 4.2e-06;
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A;Introns: 348/3; 1219/3; 1500/3; 1557/2;
A;Note: EG:87B1.2
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A;Residues: 1-1741 <MUR>
A;Cross-references: EMBL:Z98269; NID:e1355202; PID:e1251076;
C;Genetics:
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Best Local Similarity
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 LQLDKLKAGP-----HGGSKLSNALKNQNNQAAAAAAAAAAAAAAAAATPNGLK---LPLFE
                                                                     VEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANK
                                                                                                                                      IGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSL
                                                                                                                                                                                                               LLTSSSSSIQKWMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKI 715
                                                                                                                                                                                                                                                      QATL---
                                                                                                                                                                                                                                                                                       PGGLVGGHHHPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNS
                                                                                                                                                                                                                                                                                                                       ETRTRGRAKGADATTAAISPPTGKRNTRGTRGSRKAEQEVDMEVDEMAMTTVPANEEQLE
                                                                                                                                                                                                                                                                                                                                                                                             VLRGEVPRLNGNTD------PEPTEEEDQQQQPKRATRGRGRKANNNVDVTPPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYCTVKISPDKPPKERLKLIIKTDVIRNAIAKAAAAA---ESRSEKKSRSKKHKH--KQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSRLVSTDS----EEPPSSSPAHQNQLNQLSVTEEEPAERSGDETVPASTPKIT---VKPL
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                                                                                                                                                                             -LASVNNNINKIAAN-----LSAKAEASRLAEGGVA-----GGAARSYGRKRKNQQVTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GEDVDRGSPKMGRHPACGNASANQGAPA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATAT-SSSTSNSHIHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SIPLDANVLLHTLML---AAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLN
                                                                                                                                                                                                                                                  --PPRRGRNAAARANNNN------------
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19.1%; Pred. No. 2.8
                                                                                                       QQE-----PVPEEQETPDAEE-----EQPTPAK-----
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                                    - I PHTD-----HREHSPDHDPDPDELSNNSNNSS
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A;Title: A two-component histidine kinase gene that fun A;Reference number: S71629; MUID:96324397; PMID:8670894
A;Accession: S71629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: dhkA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-2150 <WAN>
A;Cross-references: EMBL
A;Experimental source: s
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C;Date: 29-Jan-1998 #sequence_revision
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                                                                                                                                                                                                                                                HIPQQLYQKQQQQQHSHSYGNHSFIHNVSPTSPSYDINNNNNNNN------NNNNNNNN
                                                                                                                                                                                                                                                                                                                                                        LVANSGGIMNEG-LLNLLSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQQQQHVAAYRH
                                  ----GNNNNNITDSPT--KSKRHSTYETNIGSHQRRKSIQSLIANSAIHSFSKLKNKPLS
                                                                 KIIGGTDTSRFGASPNLLSQQHHSAHHL----THQQQQ--QQLSAQEALGKGTRPKR----
                                                                                                    NYLNNSSSLHNINOSVNSLSNNNNNNQTNOQPINNNNNNNNNNNNNNNNNSNNSNNSNNSNNNNN--
                                                                                                                                        LLTSSSSSIQKMMAS--NIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVA
                                                                                                                                                                           RLP----KSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLN
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   ------GKYRN--
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       4.6%; Score 279; DB 2;
18.2%; Pred. No. 4.3e-06;
vative 144; Mismatches 323
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---YDR--DSLVEAVKAVQRGEMSVHRA 792
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parallel sister chromatids protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13349
R;Gandhi, R.L.; Goldberg. M T.
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A; Residues: 1-1768 <GAN>
A; Cross-references: EMBL
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                                                                                                                         LKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQ----
                                                                                                                                                             TSRLVSTDS----EEPPSSSPAHQNQLNQLSVTEEEPAERSGDETVPASTPKIT---VKPL
                                                                                                                                                                                              AAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIASAVTPTTSEVSAAAISPA
                                                                                                                                                                                                                                    TFGSPGSEPSLPPPTSAPSASASTSSQLPS---ASGSASNPPSASRTPEHPPIVLRISKG
                                                                                                                                                                                                                                                                      HDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLELYKLLTOR
                                                                                                                                                                                                                                                                                                                                   PGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATAT-SSSTSNSHIHQ
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                 NYCTVKISPDKPPKERLKLIIKTDVIRNAIAKAAAAA---ESRSEKKSRSKKHKH--KQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%; Score 282.5; DB 2; llarity 19.4%; Pred. No. 2.3e-06; Conservative 160; Mismatches 467;
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                                                                                       ----GSSAAVGGASAGDSFEERKSQSLEPNEDEEEEEEEEEEEPPEI
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                                                   ---DVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQ 378
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             parallel sister chromatids protein - fruit fly (Dr C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 (Accession: T13610 R:Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A;Description: Sequencing the distal X chromosome A;Reference number: Z17668 A;Accession: T13610
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                                                                                                                                                             fruit fly (Drosophila melanogaster)
                                                                                                                         13-Aug-1999
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                                                      QAM--DLVKSH--LMIAVREEVE 1068
                                                                                  EAMRNPOASNHHGLMKSAODMVE
                                                                                                            TAALAAAFATGAAAAATGATSAAAATQQQIQQIQQQPNAESETESASGTSAVAID-NKIE 1049
                                                                                                                                       AAAAAAAAA -- AAAAAT PNGLKLPLFEAGPQALSFQPNMFWPQTNA -- TNAYGLDFNRIT
                                                                                                                                                                    QQQHQEEQQQQPQQQQPLPPANIASASANNSNLNLTNTNV-VATGEATTNALTLTDEQA
                                                                                                                                                                                               EYKVKERHLMRP-RKREPKPQPDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQA
                                                                                                                                                                                                                         AAAAAAAAGGTAA-----TSVAAPQAIP--TLQLQSAPSTIADPQQLMVPQQQQ
                                                                                                                                                                                                                                                                                   QQAAAAANATSAVTAPPPQQTSNTSNAAVTTGQGQTMPLLS-----HMTSYEQQQPNLG
                                                                                                                                                                                                                                                                                                            DCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQL-
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                                                                                                                                                                                                                                                       -SAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYG-----VPHSTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FDSVNANAASSPNPAGDPNNMDYARTAAMQLHQTLQQLKQREDAMDVP----
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R; Frommer, G.; Vorbrueggen, EMBO J. 15, 1642-1649, 1996 A; Title: Epidermal egr-like A; Reference number: S69205; A; Accession: S69205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-1180 <FRO>
A;Cross-references: EMBL:U42403; NID:g1147788; PIDN:AAB02355.1; PID:g1147789
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es 236; Conserv
QQQQQQ------QQQQHMSSPQQQYQQHQILHQQQQFGYHHHHHHHHHHHHHHHSQL
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                                                    SLGYKKPSISVAKIIGGTDTSRFGASP----
                                                                                                                                                             AAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 - LRARNQTATPTQGGSPGHVAVQPSATASSGRSSASHLSLLNTSGQHSPTSS
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                                                                                                      TTSESNTECVGSPGNHTQSHQQQ-QQQLQHNNTSSSNSNCHHSH
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C;Keywords: DNA binding; homeobox; nucleus;
F;886-958/Domain: cut repeat homology <CUl>
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R;Blochlinger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N. Nature 333, 629-635, 1988  
A;Title: Primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of a product from cut, a locus invaluation of the primary structure and expression of the primary structure and expressio
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A; Residues: 1-2175 <BLO>
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  SSSLGYKKPSISVAKIIGGTDTS---RFGAS----PNLLSQQHHSAHHLTHQQQQQQLSA
                                                                                                         MLAAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGG
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ilarity 19.7%;
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                                                       -STLNGTKSLMQE------DSNGLAAVAMAAHAQHAAALGP
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Pred. No. 4.2e-07;
7; Mismatches 491;
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T13804
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A;Title: Shortsighted acts in the decapentaplegic pathway A;Reference number: Z17767; MUID:96038094; PMID:7555710
A;Accession: T13804
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T13804
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A; Residues: 1-1212 < T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  887 EAGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       985
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  160 NSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNR--ARHIAAASARATPAAATPANSLE 217
                                                                                                                                  104 TPTPGATSTPSPPPE--PIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAAT--ATSSSTS 159
                                                                                                                                                                                                                                                                                          al Similarity
235; Conserv
                                                                                51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIRKT-----LQASEGNGSAAGNGSNGSNGNGHGHGHGHGHALLDQLL---VKKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVENQLKQHQ-----HLNPEQAAAQQREREREQREREQQQR---LRHDDQDKMARLYQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KVKERHLMRPRKRE-------PKPQPDL-----VGLTGPAN 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGS-----YYGVPHSTLEY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIKRERLSADSGGSS----DEEHSASHINNNNSDLAHNKNKSGGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIARTPRETAFPSFLFSPSLFGGAAGMPGAASNA------FPAMADENMRHVFEREI 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMSEDRI---AHILSEASSLMKQSSVAQHREQERRSHGGEDSHSNEDSKSPPQSCTSPFF
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                                                                                SPTNSQASSPENSQEALPLLRRQQ-----
                                                                                                                                                                                    AASEDSGHQQQHQQQQ------QQQHQQHQQPLATTSVTAASTTSVLANQ 50
                                                                                                                                                                                                                                      AGSEDEPSQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQ--LLEEEDSENNQTSHDSSR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPPVTPHHSTPORPTKAV---LPPITOOQFDMFNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESEAATGHHSPGHHTTSILHEKLAQIKAEQVDQADQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --QRSSLEHSAGSSSCSKDGERDDAYPSS-----LHGRKSEGGGTPAPPAPPSGPGTGAG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKLQQHQQQQAAQAQFPNFSSLMALQQQVLNGAQDLSLAAAAAKDIKLNG-----
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                                                                                                                                                                                                                                                                                        4.9%; Solilarity 20.2%; Pi
Conservative 139;
                                                                                                                                                                                                                                                                                        Score 294; DB 2;
Pred. No. 3.8e-07;
99; Mismatches 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TCSSASGESVKRSGSPMGNYA 1028
                                                                                   -SAAAATVAAAAATVAATTSGTS
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                                                                                                                                                                                                                                                                                                                                            Length 1212;
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17-Nov-2000

Gaps

44;

96

GGGGGNG 1076

1196

1092

1041

984

924

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profilaggrin - human (fragments)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A35938
R;Gan, S,Q.; McBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.
Biochemistry 29, 9432-9440, 1990
A;Fitle: Organization, Structure, and polymorphisms of the human profilaggri
A;Reference number: A35938; MUID:91064347; PMID:2248957
A;Accession: A35938
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A; Residues: 1-2248 < GAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology; Keywords: EF hand; epidermis; polymorphism; tandem repeat 46-569/Region: filaggrin repeat 70-893/Region: filaggrin repeat 710-893/Region: filaggrin repeat 71074-1397/Region: filaggrin repeat 71074-1397/Region: filaggrin repeat 71074-1397/Region: filaggrin repeat
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Best Local Similarity
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                           SHDE-----DRAGHRQSADS-
                                                               NSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIASAVTPT 273
                                                                                                                                                                                                      EASTQADSSRHSQVG-------
                                                                                                                                                                                                                                             -----DSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATA 153
                                                                                                                                                                                                                                                                                                                                 SOYNHSSKEISQSNPNHCKT-----ENHRLEQQHNGSQLLEEEDSENNQTSH-----
                                                                                                                                                                                                                                                                                                                                                                                                                        YEISLERVAEECMG-----RRQWKHYQDKLTCSHLNIEEQQPIAIAGSED-----EP
                                                                                                               TSRNQGSSVSQDRDSEGQSEDSERH
                                                                                                                                                      TSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPA 213
                                                                                                                                                                                                                                                                                        SHYEQSVDRSGHSGSHHSHTTSQGRSDASHGTSGSRSASRQTRDEEQSGDGTRHSGSHHQ 691
                                                                                                                                                                                                                                                                                                                                                                             YQVSTHEQSESAHGRSAPSTRRRQGSHHDQARDSSRHSASQEGQDTIRGHPGSSRGGRQG 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 160;
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                                                                                                               HRGSAQEQSRDGSRHPG
                         ----SSQSGTRHTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324;
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                                           RESULT 4
S03170
homeotic protein cut - fruit fly (Drosophila melanogaster) C_iSpecies: Drosophila melanogaster .
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                                                                                                                                  GSSGSRSASRQTRNEEQSGDGSRHSRSHH-----HEASTQAESSRHSQAGQ 1710
                                                                                                                                                                      -LNGGSSSSSHIKCESEAATG-HHSPGHHTTSILHEKLAQIKAEQVDQADQ 1164
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                                                                                                                                                                                                                                                                                                           Q-AGPHQQAHQESARGQSGESSGRSGSFLYQVSTHEQSESTHGQSVPSTGGRQGSHHDQA 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSHHSHTTSQGRSD-ASHGQSGSGSHHQQS-----ADSSRH-----SGIGHGQASSAV 1015
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1233 696 643 1126 1073

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379 848

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1664

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1546 1021 1434

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R;Haynes, S.R.; Mozer, B.A.; Bhatia-Dey, N.; Dawid, Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect A;Reference number: A43742; MUID:89276730; PMID:256; A;Accession: A43742
                                                                                                                                                                     female sterile homeotic protein, 205K - fruit fly (
N;Alternate names: membrane protein fsh, 205K
N;Contains: female sterile homeotic protein, 110K
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993
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                    A; Molecule type: mRNA
A; Residues: 1-2038 < H
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     A;Cross-references:
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 EMBL:M23221; NID:g157452; PIDN:AAA28540.1;
                                                                                       locus, a maternal effect homeotic MUID:89276730; PMID:2567251
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1106 <HA2>
A;Cross-references: EMBL:M23222
C;Genetics:
A;Gene: fsh
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C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status pred
F;1-1106/Product: female sterile homeotic protein, 110K #status pred
F;59-116/Domain: bromodomain homology <BRO1>
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1: pir1:*
2: pir2:*
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4: pir4:*
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Dev. Biol. 171, 85-97, 1995
A;Title: The Drosophila E93 gene from the 93F early puff displays stage- ar A;Reference number: Z17648; MUID:96018744; PMID:7556910
A;Accession: T13283
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1221 <BAE>
A;Cross-references: EMBL:U25686; NID:g886047; PID:g886048; PIDN:AAA833228.1
A;Experimental source: strain Canton S
C;Genetics:

probable transcription factor E93 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C;Accession: T11283 R;Baehrecke, E.H.; Thummel, C.S.
Dev. Biol. 171, 85-97, 1995

stage- and tissue-spec

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ALIGNMENTS

361 RSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLSHL 420	Qy
301 SSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQ 360	D Qy
241 QFSLLADFNLINSLASQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTBSPSVDAPLDL 300	Qy da
181 SSSSSSNNNSSGNRARHIAAASARATÞAAATÞANSLELYKLLTQRAAKMTSMDSMAAQLA 240 	Qy da
121 DWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHI 180	Qy Ob
61 EISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTPGATSTPSPPPEPI 120	Qy
1 MHISSYEISLERVAEECMGRRQWKHYQDKLTCSHLNIEEQQPIAIAGSEDEPSQYNHSSK 60	Qy da
Query Match 80.2%; Score 4839; DB 2; Length 1221; Best Local Similarity 84.0%; Pred. No. 4.8e-234; Matches 972; Conservative 25; Mismatches 90; Indels 70; Gaps 9;	
A;Gene: E93 A;Cross-references: FlyBase:FBgn0013948 A;Map position: 3R C;Function: A;Description: probably acts in a stage-specific regulatory hierarchy in the salivary	מממחמ

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Result
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

RESULT 1 T13283

probable transcription factor E93 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Ante: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13283
R;Baehrecke, E.H.; Thummel, C.S.
Dev. Biol. 171, 85-97, 1995
A;Title: The Drosophila E93 gene from the 93F early puff displays stage- and tissue-spec A;Accession: T13283
A;Accession: T13283

A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1221 <BAE>
A;Cross-references: EMBD:U25686; NID:g886047; PID:g886048; PIDN:AAA83228.1
A;Experimental source: strain Canton S
A;Experimental source: strain Canton S

C; Genetics:

20	. 361 RSILDNRLFKMKHHDOEODHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAOLRKLSHL 420	 	
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360	301 SSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQHHEQ :	у	
300	241 QFSLLADENLINSLASQQQQQQQQAQASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDL	Db	
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240	181 SSSSSNNNSSGNRARHIAAASARATPAAATPANSLELYKLLTQRAAKWTSMDSMAAQLA	מם	
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180	121 DWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHI	da	
180	121 DWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTSNSHIHQHDSDSNSSASLPHHI	·VΩ	
120	61 EISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTPGATSTPSPPPEPI	Db	
120	61 EISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPTPGATSTPSPPPBEPI	۷۷	
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9;	Query Match 80.2%; Score 4839; DB 2; Length 1221; Best Local Similarity 84.0%; Pred. No. 4.8e-234; Matches 972; Conservative 25; Mismatches 90; Indels 70; Gaps		
e salivary gl.	C.Function: A;Description: probably acts in a stage-specific regulatory hierarchy in the	≯ .0	
	A;Gene: E93 A;Cross-references: FlyBase:FBgn0013948 A;Map position: 3R	D D D D D D D D D D	

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female sterile homeotic protein, 205K - fruit fly (Drosophila melany), Alternate names: membrane protein fsh, 205K 1; Contains: female sterile homeotic protein, 110K 2; Species: Drosophila melanogaster 2; Date: Olympia melanogaster 20-1, 2; Date: Olympia melanogaster 20
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   A; Cross-references:
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C;Superfamily: unassigned bromodomain proteins; bromodomain C;Keywords: alternative splicing; transmembrane protein F;1-2038/Product: female sterile homeotic protein, 205K #staF;1-1106/Product: female sterile homeotic protein, 110K #staF;1-1106/Product: female sterile homeotic protein, 110K #staF;59-116/Domain bromodomain homology cBR01>
F;503-560/Domain: bromodomain homology cBR02>
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A;Residues: 1-1106 <HA2>
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A;Status: preliminary
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PHGGSKLSNALKNONNOAAAAAAAAAAAAAATPNGLKLPLFEAGPQALSFOPMMFW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGSHGDAMVNASLASLASGLKQIPQFDDPVEQSLAS----LEFSAGSTGKSGLTDNFL- 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIASNLHKPSGL---GGGDLGEHHAALAAALTSGINSTG--TAGGGINNNGGSNNNANPL 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSNFGG-----APAPG----NMMHAGAGVPVAGAAVSASTGQQHN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQQQQQQQIASAVTPTT------SEVSAAAISPALKDTPSPSVDAPLDLSSKPS-P
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                                                                                          -----QQQQQQQHLQQQQHQQQHHQAANKLLIIPKPIESM--MPSPPDKQQLQQHQKVL 1600
                                                                                                                                                                                                                                                                                                                        QQQQQQTHQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRNGSNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSI-----QKMMASNIQRQIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNH----SSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFA--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDV-VANKLDARKSASQHHEQRSILD
                                                                                                                                                                                                                                                              AHHLTHQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYG
                                                                                                                                                                                                                                                                                                                                                                               EQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHS 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- PANYLLHTLMLAAGIGAMPKLDE--TQTVGDFIKGLLVANSGGIMNEGLL-NLLS 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- RAQLRKLSHLSEHNGSDLGED------VDRGSPKMGRHPACGNASANQGAPASI-PL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KNGPNDLSKVQPGGPI------NAALP--PHSFAGGTATVATSQSSGGI 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GALSPTTMLMGLDHVVNSNTPTSQMSNMLGNANPLTAAAMLNNNNKTSLP
                                                                                                                                              VPHSTLEYKVKERHLMRPRKRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DYVTEL-----LSKGAENVGGMNG--NHLLNFNLDMAAAYQQKHPQQQQQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RPPRKKKSRDSNGSNVNNPSI----NVVMGGNLPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                           VADFGMAGFDGLNMTAASFLDLEPSLQQQQMQQMQLQQQHH 1513
                                                                                                                                                    ---PKPQPDLVGLTGPANKLQLDK-LKAG 844
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RESULT 4 \$03170 homeoric protein cut - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster	QY 214 NSLELYKLLTORAAKHTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQIASAVTPT 273
Oy 1116 -LNGSSSSSHIKCESERATG-HHSPGHTTSTLHEKLAQIKAEQVDQADQ 1164	Oy 154 TSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPA 213
160	QY 100DSSRTPTPGATSTPSPPPEPIDWRPSAKCNECVNGRLLTVNAQGKLVAESAATA 153
1022 SPMGNYADIKRERLSADSGGSSSELSASHINNNNSDLAHKNKKSGGGGGGG	QY 53 SQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSH 99
979	QY 6 YEISLERVABECMGRQWKHYQDKLTCSHLNIEEQQPIAIAGSEDEP 52
929 HHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNGSNGNGHGHGH	5.0 rity 19.0 nservative
Qy 877 TPNGLKLPLFEAGPQALSFQPNMFWPQTNATNAYGLDENRITEAMRNPQASN 928	on: filaggrin repeat no: filaggrin repeat jion: filaggrin repeat
Qy 817 KREPKPOPDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNONNOAAAAAAAAAAAAAAAAAAA 876 : : : : :	A;Cross-references: GDB:119912; OMIM:135940 A;Map position: 1q21-1q21 C;Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology C;Keywords: EF hand; epidermis; polymorphism; tandem repeat
QY 757 GKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPR 816	: 1-22 ferences
Qy 697 NGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEAL 756	A35938; MUID:91064347; PMID:2248957 (ry; not compared with conceptual translation
Qy 644 AVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSN 696	.W.; Idler, W.W.; Markova, N.; Steinert, P.M. 440, 1990 structure, and polymorphisms of the human profil
Qy 584 KVSGPASSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAA 643	35938 rofila ;Speci
Qy 524 LLLQQQQHQQHHQQHQQQQQQQHVAAYRHRLPKSETPETNSSLDPNDASEDPILKIPSF 583	Db 1843 ANSNSGGGGGGPALLNAGSNSNSGVGSGGAASSNSNS 1881 RESULT 3
QY 482 DETQTVGDFIKGLLVANSGGIMMEGLLNLLSAS	1/9/ QSGGGGGT 1842 1098 SSFKSGENGGQQNHKMMDLNGGSSSSSHIKCESEAATGHHS 1138 ::
969 GSHHSHTTSQGRSD-ASHGQSGSGSHHQQSADSSRHSGIGHGQASSAV	1043 SDEEHSASHINNNNSDLAHNKNKSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Db 909 GRTRTSTGRRQGSHHEQARDSSRHSASQEGQDTIRAHPGSRRGGRQGSHHEQSVDRSGHS 968 Oy 425 GSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLHTLMLAAGIGAMPKL 481	QY 983 ALLDQLLVKKTPLPFTNHRNNDYAATCSSASGESVKRSGSPMGNYADIKRERLSADSGGS 1042
Db 849 SDQEGHSEDSDSQSVSAQROAGSHQQSHQESTRGRSQGRSGSFIYQVSTHEGSESAH 908 QY 380HDGDELEDSNDDAEAEVDSNASTPYYPAEFARAQLRKLSHLSEHN 424	Qy 926 ASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGH 982
334 EDLSRALQDVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQD	:: :: ASANSPOSHTSSSSSSSKAKPAMDSFQOFRNKAKERDRLKLLEAAEKEKKNQKEAAEKEQ
QY 274 TSEVSAAAISPALKDTPSPSVDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSE 333	Db 1601 PPQQSPSDMKLHPNAAAAAVASAQAKLVQTFKANEQNLKNASSWSSL 1648

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 (;Accession: S03170 R;Blochlinger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N. Nature 333, 629-635, 1988
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A;Residues: 1-2175 <BLO>
A;Cross-references: EMBU:X07985; NID:g7767; PIDN:CAA30794.1; PID:g7768
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A;Cross-references: FlyBase:FBgn0004198
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                                                                        MLAAAVAQGGYSAGNSLLTSSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNNNGQ------PAVLLAAKDKEIKALLDELQRLRAQEQT------HLVQIQ 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVNAQGKLVAESAA-----TATSSSTSNSHIHQHDSDSNSSASLPHHISSSSSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQQQHQQQ--DTEDLEENKDAGEASLNVSNNHNTTDSN------NSCSRKNNN 364
SSSLGYKKPSISVAKIIGGTDTS---RFGAS----PNLLSQQHHSAHHLTHQQQQQQLSA
                                     QLASLA----STLNGTKSLMQE-----DSNGLAAVAMAAHAQHAAALGP
                                                                                                             ----GHHLHGHGLLHPSSAHHLHHQTTESNSNSSTPTAAGNNNGSNNSSSNTNANSTA
                                                                                                                                              PGGLVGGHH------HPLNNNNSLSISNNSNHSSNSHRNGSNRSPH----SASP 639
                                                                                                                                                                                                                        QQHHQQQQQQHVAAYRHRLPKSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLS
                                                                                                                                                                                                                                                             AAAAAACANDPNKF-QALLIERTKALAAEALKNGASDALSEDAHH-----QQQQHHQQQ
                                                                                                                                                                                                                                                                                                AMPKLDETQTVGDFIKGLLVANSGGIMNEGLLNLLS-ASQENSNGNASLLLQQQQHQQHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167; Mismatches 491;
                                                                                                                                                                                   -HLQQQPNSGSN------SNPASNDHHH
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R;Treisman, J.E.; Lai, Z.C.; Rubin, G.M. Development 121, 2835-2845, 1995
A;Title: Shortsighted acts in the decapentaplegic pathway A;Reference number: Z17767; MUID:96038094; PMID:7555710 shs protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T13804 A;Molecule type: mRNA A;Residues: 1-1212 <TRE> A;Cross-references: EMBL:L42512; NID:g833709; PID:g833710; PIDN:AAC41608.1 A;Status: preliminary; translated from GB/EMBL/DDBJ 1093 LIARTPRETAFPSFLFSPSLFGGAAGMPGAASNA-----FPAMADENMRHVFEREI 1143 104 TPTPGATSTPSPPPE--PIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAAT--ATSSSTS 925 LSKPKPWDKLTEKGRDSYRKMHAWACDDNAVMLLKSLIPKKDSGLPQYAGRGAGGADD 871 QEML----RYNMDKYANQALDTL--HISRRVRELLSVHNIGQRLFAKYILGLSQGTVSEL 924 160 NSHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNR--ARHIAAASRATPAAATPAASLE GFLPGLPAFQFAAAQVAAGGDGRGHYRFADSELQLPPGASMAGRLGESLIPKGDPMEAKL SPTNSQASSPENSQEALPILERRQQ-----SAAAATVAAAAATVAATTSGTS LPFTNHRNNDYAA-------TCSSASGESVKRSGSPMGNYA 1028 IIRKT-----LQASEGNGSAAGNGSNGSNGHGHGHGHGHALLDQLL---VKKTP KVENQLKQHQ-----HLNPEQAAAQQREREREQREREQQQR----LRHDDQDKMARLYQE EAGPOALS FOR IMFWROTINA TINAY GLDFINR I TEAMRIN POAS NIHIGLMKS A QDMVEN VYDG SMSEDRI---AHILSEASSLMKQSSVAQHREQERRSHGGEDSHSNEDSKSPPQSCTSPFF QEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGS-----YYGVPHSTLEY-AASEDSGHQQQHQQQQ------QQQHQQHQQHQQPLATTSVTAASTTSVLANQ AGSEDEPSQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQ--LLEEEDSENNQTSHDSSR 103 TQPPVTPHHSTPQRPTKAV---LPPITQQQFDMFNNL 1339 ESEAATGHHSPGHHTTSILHEKLAQIKAEQVDQADQL 1165 APPTAAPPTGGASSNSAAPSPLSNSILPPALSSQGEEFAATASPLQRM----ASITNSLI 1305 -----QTNG-NGRSSRMTSRDDSETDASSFKSGENGGQQNHKMMDLNGGSSSSSHIKC -- ORSSLEHSAGSSSCSKDGERDDAYPSS-----LHGRKSEGGGTPAPPAPPSGPGTGAG DIKRERLSADSGGSS---DEEHSASHINNNNSDLAHNKNKSGGG-----GGGGGGNG KLQLDKLKAGPHGGSKLSNALK-----NQNNQAAAAAAAAAAAAAAATPNGLKLPLF 4.9%; Score 294; DB 2; lilarity 20.2%; Pred. No. 3.8e-07; Conservative 139; Mismatches 421; #text_change 17-Nov-2000 Length 1212; Indels 368; ä Drosophila eye development Gaps 1076 1196 1092 217 159 50 1249 994 946 1041 886 984 96

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                                                                                                                                  AAAAAAAA---AAAAATPNGLKLPLFEAGPQALSFQPNMFWPQTNA--TNAYGLDFNRIT 918
                                                                                                                                                              QQQHQEEQQQQPQQQQQPLPPANIASASANNSNLNLTNTNV-VATGEATTNALTLTDEQA
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                                                    QAM--DLVKSH--LMIAVREEVE 1068
                                                                          EAMRNPQASNHHGLMKSAQDMVE 941
                                                                                                       TAALAAAFATGAAAAATGATSAAAATQQQIQQLQQQPNAESETESASGTSAVAID-NKIE 1049
                                                                                                                                                                                                                                              -SAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYG-----VPHSTL 803
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A;Molecule type: mRNA
A;Residues: 1-1180 <FRO>
A;Cross-references: EMBL:U42403; NID:g1147788; PIDN:AAB02355.1;
C;Keywords: alternative splicing
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EMBO J. 15, 1642-1649, 1996
A;Title: Epidermal egr-like zinc finger protein of Drosophila participates in myotube
A;Reference number: S69205, MUID:96203082; PMID:8612588
A;Accession: S69205
A;Status: preliminary; nucleic acid sequence not shown
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C;Species: Drosophila melanogaster
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 DLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVLLH--TLMLAAGIGAMPKLDET 484
                                                                               606 QQQQQ------ОQQQНМSSPQQQYQQHQILHQQQQFGYННННННННННННКQL
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    -QQQQQQLSAQEALGKGTRPKRGKYRNY-----
                                                                                                                                                                                                                                           TTSESNTECVGSPGNHTQSHQQQ-QQQLQHNNTSSSNSNCHHSH
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--- DRDSLVEAVKAVQR 784
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A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: Z17668 A;Accession: T13610 A;Status: preliminary; translated from GB/EMBL/DDBJ	Qy 342DVVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQ 378	p 9
n: T13610 L; Harris, D; Barrell, B. to the EMBL Data Library, April 1999		D 5
C.Date. 13-Aug-1999 #segmence regision 13-Aug-1999 #text change 17-Nov-2000	Oldas luassavadausalautava ansamuus losmasanss lula aunos deliki. Itusi emaa luassavadan andalauta emaan seesa ansamuus lusus	2 5
n	QY 226 AAKMTSMDSMAAQLAQFSLLADFNLINSLASQQQQQQQQQQIASAVTPTTSEVSAAAISPA 285	ŞŞ
Db 1168 MDDDVEYILDALQPHNPPATRCLSAL 1193	293 TFGSPGSEPSLPPPTSAPSASASTSSQLPSASGSASNPPSASRTPEHPPIVLRISKG	D
Qy 1122 SSSHIKCESEAATGHHSPGHHTTSIL 1147	166 HDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLELYKLLTOR	Ş
1117	UY 107 PGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATAT-SSSTSNSHIHQ 165 Db 259 PTKDLIIPKAGRQPAPVATATLAAASSEAFISS 292	B ĉ
	203 ASEQPEOPSSASGKOKOKKPKEEKKLKPEAPPSRVLGRARKAVNYREVDEDERYPT 258	
1025	NHCKT	ð
: : :	Query Match 4.7%; Score 282.5; DB 2; Length 1768; Best Local Similarity 19.4%; Pred. No. 2.3e-06; Matches 238; Conservative 160; Mismatches 467; Indels 361; Gaps 45;	
969 SNGNGHGHGHGHGHALLDQLLV	A;Cross-references: FlyBase:FBgn0004655	Α;
990	,	» C:
Qy 909 AYGLDENRITEAMRNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNG 968	A;Residues: 1-1768 <gan> A;Cross-references: EMBL:U40214; NID:gl100982; PID:gl100983; PIDN:AAA91230.1</gan>	D D
Db 930 KRTLTLDTQGAANAGAGGAAAAAPPESSGEQRGAVKLVISKKKGSIFKSRALVPSDQAEQ 989	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	Α;
09 852 SNAĻKNQNNQAAAAAAAAAAAAATPNGLKLPĻFEAGPQALSFQPNMFWPQTNATN 908	57	A .
Db 879 -IPHTDHREHSPDHDPDPDPDELSNNSNNSSLQHDGSSSSPPPRDFKFKDKF 929	R;Gandhi, R.L.; Goldberg, M.L. submitted to the EMBL Data Library, November 1995	su.
Qy 797 GVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGPHGGSKL 851	C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C;Accession: T13349	ຕູ
Qy 737 SAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHKAGSYY /96	osophila melan	Da C;
SAKAEASRLAEĠĠŸĀGĠAARŚŸĠRKKNQQŸTQVLQQE-	RESULT 7	R E
Qy 677 NEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHH 736	1003 TVPL 1006	
Db 766 DMEVDETAMTTVPANEEQLEQATLPPRRGRNAAARANNNNLASVNNNINKIAANL 820	へ・ 993 T-PL 995	?
Qy 630 SNRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQI 676	0b 948MQPS-SNGTGYSGGSGGSSAAAAAAAAAAAAAVQLABYSPSTSKGHEILSQVYQQS 1002	90
Db 721 TPPATETRTRGRAKGADATTAAISPPTGKRNTRGTRGSRKAEQEV 765	948 IRKTLQASE	δ
QY 570 NDASEDPILKIPSFKVSGPÄSSSSLSPGGLVGGHHHPLNNNNSLSISNNSNHSSNSHRNG 629	892 WLDSPADYAQQQQVQQVQQQQQQQTLVLPGPTSS	망
Db 677 VLRGEVPRLNGNTDPEPTEEEDQQQQPKRATRGRGRKANNNVDV 720	Qy 901 WPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGI 947	γQ
510 LLSASQENSNGNASLLLQQQQHQ		da
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457SIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLN	GLPSPDKTMFQPPLFSLPAHYATMQQQQQQQQQQQQQQQQQQQQQAAGAABSPYDDGRAAAAA	g 3
574 ISPTTRSDHDFDSOSSVLGSISSKGNSTPQLLAQAVQEDSCVIRSRGSSVITSDLETSQH	837OLDKIKAGPAAAAA	ر د
429GEDVDRGSPKMGRHPACGNASANQGAPA	714 GIFTTTGNAMNAAAAAAAAAAAAOOHOOOOHOOOLPSPOLGVLAGPMSPPSNSLGNSW	B 4
Db 514 LAAGSGAAPASGATPAEINSEFKTPSPHLALSEANSOOAOHTPSHLHOLHOLHPORGSAV 573	DD 785 GEMSVHRAGSYYGVPHSTLEYKVKERHIMRPRKREPKPOPDLYGLTGPANKL 836) ;
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A:Introns: 348/3; 1219/3; 1500/3; 1557/2; 1587/1; 1650/3
A:Note: EG:87B1.2
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A;Residues: 1-1741 <MUR>
A;Cross-references: EMBL:298269; NID:e1355202; PID:e1251076; PIDN:CAB10973.1
C;Genetics:
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836 LQLDKLKAGP-----HGGSKLSNALKNQNNQAAAAAAAAAAAAAATPNGLK---LPLFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 SEDEPSQYNHSSKEISQSNPNHCKTENHRLEQQHNGSQLL-EEEDSENNQTSHDSSRTPT
                                                                                                                                                                                                                                                     QATL----PPRRGRNAAARANNNN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSLVAPPSDIESRLESMMMTIDGAGTGAASAVPETP------LQEDILA
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                                                                                                                                     IGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSL
                                                                                                                                                                                                            LLTSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVAKI 715
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                                                                  VEAVKAVQRGEMSVHRAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANK
                                                                                                                                                                                                                                                                                                                      ETRTRGRAKGADATTAAISPPTGKRNTRGTRGSRKAEQEVDMEVDEMAMTTVPANEEQLE
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                                                                                                                                                                           -LASVNNNINKIAAN-----LSAKAEASRLAEGGVA-----GGAARSYGRKRKNQQVTQV
                                                                                                                                                                                                                                                                                                                                                        ET-----PETNSSLDP------NDASEDPILKIPSFKVSG-PASSSSLS
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                                   -----IPHTD-----HREHSPDHDPDPDPDELSNNSNNSS
                                                                                                        QQE----PVPEEQETPDAEE----EQPTPAK--
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C;Superfamily: response regulator homology
C;Keywords: autophosphorylation; phosphoprotein; phosphotransferase;
F;2027-2142/Domain: response regulator homology <RRH>
F;2076/Binding site: phosphate (Asp) (covalent) #status predicted
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A;Cross-references: EMBL:U42597
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A; Accession: $71629
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative 144;
                                                                                                                                                                                                                                                                                                                                                                                                          4.6%; Score 279; DB 2; Length 2150; 18.2%; Pred. No. 4.3e-06;
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1045 EEHSASHINNNNSDLAHNKNKSGGGGG--GGNGQTNGNG--RSSRMTSRDDSETDASSF 1100
                                                                                                                                                                                                                                                                                                                                                                   1005 YAATCSSASGESVKRSGSP-MGNYADIKRERLSADSG-------GSSD 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 -----AALEANG--GGTNSDASNASASGVGVAGAKDHLHHLAAGKSDGDFGDSPSSNNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  888 AGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGI
                                                                    KSGENGGQQNHKMMDLNGGSSSSSHIKCESEAATGHHSPGHHTTSIL 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOHDGSSSSPPRRDFKFKDKFKRTLTLDTQGAANAGAGGAATAAPPESSGEORGAVKLVI
KTA-----HQIQEIGEYQEMDDDVEYILDALQPHNPPATRCLSAL 1193
                                                                                                                                                                                                                                                                                          SSSACSSA---STLRGDSPALG-----KISRLAGKQGVPATSTSSDAFDLDLEPIAGELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRKTLQASEGNGSAAGNGSNGSNGNGHGHGHGHGHALLDQLLVKKTPLPF---TNHRNND
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                                                                                                                                                 ----GASAGGTGATTGGGGATGGGGPIRVDRKTK--DYYPVVRNV 1153
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sensory transduction histidine kinase dhkA - slime mold (Dictyostelium disco C;Species: Dictyostelium discoideum C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 24-Sep-1998 C;Accession: \$71629 R;Wang, N.; Shaulsky, G.; Escalante, R.; Loomis, W.F. EMBO J. 15, 3890-3898, 1996 A;Title: A two-component histidine kinase gene that functions in Dictyostelium developme A;Reference number: S71629; MUID:96324397; PMID:8670894 (Dictyostelium discoideum)

two-component regula

765 609 NNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQG-------GYSAGNS 554 RLP-----KSETPETNSSLDPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHHPLN 495 LVANSGGIMNEG-LLNLLSASQENSNGNASLLLQQQQHQQHHQQHHQQQQQQQQHVAAYRH ----GNNNNNITDSPT--KSKRHSTYETNIGSHQRRKSIQSLIANSAIHSFSKLKNKPLS 291 KIIGGTDTSRFGASPNLLSQQHHSAHHL---THQQQQ--QQLSAQEALGKGTRPKR----LLTSSSSSIQKMMAS--NIQRQINEQSGQESLRNGNVSDCSSNNGGSSSLGYKKPSISVA 713 HIPQQLYQKQQQQQHSHSYGNHSFIHNVSPTSPSYDINNNNNNNN------NNNNNNNNN YDR - - DSLVEAVKAVQRGEMSVHRA Indels 164; Gaps 237 655 120 309 67 764 27

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DLSRALODVVANKLDARKSASOHH	_change	Oy	DIAHNKKKSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SFFILHDPODYHLOSGAGSVRGLRLOQUCCTAWQSFRILDPODYHLOSGAGSVRGLRLOQUCCTAWQSRALQDVVAI SFFILHDPODYHLQSGAGSVRGLRLQOQCCTAWQDGSGSDESVS.I. LISSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVAI SERPPAATVESGORYDHQADVTPAPADGSGSDESVS.I. EQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVY. ARRVSIATVAAATSAPATVAAATSAP HLSEHNGSDLGEDVDRGSPKMGRHPACGNASANQGAPASIPLDANVL. NIKNNNYKVTRASP
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A;Cross-references: FlyBase:FBgn0000630
A;Introns: 56/2; 117/3; 177/3; 577/3; 730/3; 838/1; 1014/2; 1134/3; 1217/3; 1287/2
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
F;63-96/Domain: ankyrin repeat homology <AN1>
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A;Molecule type: DNA
A;Residues: 1-1449 <HOO>
A;Cross-references: EMBL:X69871
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Best Local Similarity
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                                                                                                                                                                                                      CSSNNGGSSSLGYKKPSIS-VAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                     QQQQQQQQQQQLQHKYNVGRSRSRDSGSH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIKNNN----YKVTRASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTPVYPAEFARAQLRKLS
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                                                                                                                                                                                                                                                      SKYESCLKDNYSAKNVNLKNQLLNGGIKSDTYESVCPPEDVAERTKQTHKNSMIRNNLAD
                                                                                                                                                                                                                                                                                              --AAAVAQGGYSAGNSLLTS-----SSSSIQKMMASNIQRQINEQSGQESLRNGNVSD
                                                                                                                                                                                                                                                                                                                                           DIVLOYSNHH--LNNKRNMNNNSNMNNSSSNIAOSSSSSNNNNNSLLNRNKSHSIIGLHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TTT-----EDIYLVREESRKQHQQQQQHQLQQQQQLQHQATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLL----ADFNLINSLASQQQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSNNNSSGNRARHIAAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNPNHCKTENHRLEQQHNGSQLLEEEDSENNQTSHDSSRTPT--PGATSTPSPPPEPIDW
ERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGPHGGSKLSNALKNQNNQAAAA----
                                                                  ---AVVNGPPP------PPLPPPLRAPVQQQRNNLSVDQPNS---------
                                                                                                                                                         ASSNNNTSGSIN----NISNIGNMNGGNQSSR-----NLKRVSSAPPMQNL-
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                                                                    761
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A;Cross-references: FlyBase:FBgn0008654
A;Introns: 55/1; 139/2; 219/3
A;Introns: 55/1; 139/2; 219/3
C;Superfamily: Drosophila suppressor protein of C;Keywords: DNA binding; nucleus; zinc finger F;31-79/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-612,614-784,'N',786-830,'R',832-965,967-1064,'E',1066-1096,'N',1097-1286,
A; Residues: 1-612,614-784,'N',786-830,'R',832-965,967-1064,'E',1066-1096,'N',1097-1286,
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
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A; Residues: 1-1365 < MBRUs
A; Residues: 1-1365 < MBRUs
A; Cross-references: EMBL: X56799; NID: g8528; PID: g8529
A; Cross-references: EMBL: X56799; NID: g8528; PID: g8529
A; Brunk, B.P.; Adler, P.N.
Nucleic Acids Res. 19, 3149, 1991
Nucleic Acids Res. 19, 3149, 1991
A; Title: The sequence of the Drosophila regulatory gene
A; Reference number: $16845; MUID: 91279476; PMID: 2057369
A; Accession: $16845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suppressor two of zeste protein - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-JuC;Accession: S14871; S16845
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                                                                                                                                                                                                      LLTQRAAKMTSMDSMAAQL------262
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                                                                    AEDFELKTANRKGVGHLPKLKIELNSMKSKLSMPLSA---GPRLEDTSCSSSCSAQQLDL
                                                                                                                                                         SL--RSNDMRYSDYAVSKVKSEPEQEQFLLPREREQQPLEANTNIVVSIPPSQLRKSYVD 377
                                                                                                                                                                                                                                                      SEIDSGSPRSKVRCKTPPKVSPSSKNKRLTSSKR--
                                                                                                                                                                                                                                                                                              SHIHQHDSDSNSSASLPHHISSSSSSNNNSSGNRARHIAAASARATPAAATPANSLELYK 220
                                                                                                                                                                                                                                                                                                                                           NWSRESPMAFCY -- RILLYDNEQTKNDENNLSRINQDIEPEHSVRRSKSAKSVTFAEDLE 273
                                                                                                                                                                                                                                                                                                                                                                                        DWRPSAKCNFCVNGRLL-----TVNAQGKLV-----AESAATATSSSTSN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSADSGGSSDEEH 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGSTNGSSIAASSDDS-QSRYGGSVH-----AANGSAANGHFYGYSEGNKNQGSNANGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAA------GNGSNGSNGNGH 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AAAAAAAAAATPNGLKLPLFEAGPQALSFQPNMFWPQTNATNAYGLDFNRITEAMRN 923
                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%; Score 271; DB 2; ilarity 19.7%; Pred. No. 6.2e-06; Conservative 154; Mismatches 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GGSSAEDH
                  -VDAPLDLSSKPSPNSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          940
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                                                                                                               QQQIASAVTPTTSEVSAAAISPALKDTPSPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NYHSHPNQPHYAT----GQPHQYTPSLYG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                suppressor two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zeste; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1365;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of zeste encodes
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	Qy 735 HHSAHHLTHQQQQQQLSAQEALGKGTRPKRGKYRNYDRDSLVEAVKAVQRGEMSVH 790	Z 🛭	C;Spi C;Dai C;Aco
	Oy 689 NVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQ 734	JLT 13	RESULT S52714 Serici
	Qy 631 NRSPHSASPMLAAAVAQGGYSAGNSLLTSSSSSIQKMMASNIQRQINEQSGQESLRNG 688	1129 ESEAATGHHSPGHHTTSILHEKLAQIKAEQ 1158 :: ; ; ; ; ; ; ; ; ; ;	유
	Qy 571 DASEDPILKIPSFKVSGPASSSSLSPGGLVGGHHPPLNNNNSLSISNNSNHSSNSHRNGS 630	1071 GGGGNGOTNGNG-RSSRMTSRDDSETDASSFKSGENGGOQNHKMMDLNG-GSSSSSHIKC 1128	ğ X
	Qy 511 LSASQENSNGNASLLLQQQQHQQHQQHQQQHQQQHVAAYRHRLPKSETPETNSSLDPN 570	1026 NYADIKRERLSADSGGSSDEEHSASHINNNNSDLAHNKNKSGGGG 1070	qu
	Oy 452 OGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGG-IMNEGLLNL 510	969 SNGNGHGHGHGHALLDQLLVKKTPLPFTNHRNNDYAATCSSASGESVKRSGSPMG 1025	?
	Qy 404 VYPAEFARAQ	909 AYGLDFNRITEAMRNPQASNHHGLMKSAQDMVENVYDGIIRKTLQASEGNGSAAGNGSNG 968	da Vc
	Qy 358 HEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVDSNASTP 403	854ALKNONNOAAAAAAAAAAAAATPNGLKLELFEAGPQALSFQDNMFWPQTNATN 908	D Qy
	Qy 307 NSSISGDVKSVRACATPTPSGRRAYSEEDLSRALQDVVANKLDARKSASQH 357	812 LMRPRKREPKP	4G AC
	Qy 247 DFNLINSLASQQQQQQQQIASAVTPTTSEVSAAAISPALKDTPSPSVDAPLDLSSKPSP 306	754 EALGKG-TRPKRGKYRNYDRDSLVEAVKAVQRGEMSVHRAGSYYGVP-HSTLEYKVKERH 811	4a Ac
	QY 199 AAASARATPAAATPANSLELYKLLTQRAAKMTSMDSMAAQLAQFSLLA 246	694 SSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQQQQQLSAQ 753	do 40
	Qy 155 SSSTSNSHIHQHDSDSNSSASLPHHISSSSSSNNNNSSGNRARHI 198	658 TSSSSSIQKMMASNIQRQINEQSGQESLRNGNVSDC 693	P Q
	Qy 98SHDSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRULTVNAOGKLVAESAATAT 154	604HHPLNNNNSLSISNNSNHSSNSHRNGSNRSPHSASPMLAAAVAQGGYSAGNSLL 657	
	Qy 57 HSKEISQSNPNHCKTENHRLEQQHNGSQLLEEEDSENNQT 97	568 DPNDASEDPILKIPSFKVSGPASSSSLSPGGLVGGH	dg VC
	Qy 5 SYEISLERVAEECMGRRQWKHYODKLTCSHLNIEEQQPIAIAGSEDEPSQYN 56 : : :	510 LLSASQENSNGNASLLLQQQQHQOHHQQHQQOQQQHVAAYRHRLPKSETPETNSSL 567	ρ γ
	Query Match 4.5%; Score 270.5; DB 2; Length 1217; Best Local Similarity 18.5%; Pred. No. 5.7e-06; Matches 238; Conservative 174; Mismatches 483; Indels 389; Gaps 45;	450 ANQGAPASIPLDANVLLHTLMLAAGIGAMPKLDETQTVGDFIKGLLVANSGGIMNEGLLN 509	da VC
f the fo	R;Garel, A.A.; Deleage, G.G.; Prudhomme, J.J. submitted to the EMBL Data Library, March 1995 A;Description: Structure and organisation of the Bombyx mori sericin I gene and of A;Reference number: S52714 A;Accession: S52714 A;Status: preliminary A;Molecule type; mRNA A;Residues: 1-1217 <gar> A;Cross-references: EMBL:Z48802; NID:g755699; PID:g755700</gar>	435 ETYAKNIGLKPIEQPLQQSAS-NPDSKYSPNASPMSSCSSSTNGSSSSLGTADASTS 490 343 VVANKLDARKSASQHHEQRSILDNRLFKMKHHDQEQDHDGDELEDSNDDAEAEVD 397	40 40 40 40

Qy 100 DSSRTPTPGATSTPSPPPEPIDWRPSAKCNFCVNGRLLTVNAQGKLVAESAATATSSSTS 159	Oy 1066 SGCGGGGGGGNGOTNGNGRSSRMTSRDDSETDASSFKSGENGGQONHKNMDLNGGSSSSSH 1125	Qy 791 RAGSYYGVPHSTLEYKVKERHLMRPRKREPKPQPDLVGLTGPANKLQLDKLKAGPHGG 848
RESULT 15 S66149 S66149 Gene pipsqueak protein A long form - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 23-Sep-2002 C;Accession: S66149; S66150; T45461 R;Weber, U.; Siegel, V.; Mlodzik, M. EMBO J. 14, 6247-6257, 1995 A;Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up for tl A;Accession: S66149 A;Accession: S66149 A;Accession: S66149 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1085 <web></web>	Db 1444 SLSDSTSISKSTSQSGSTSTSASESTSESAST 1493 Qy 626 HRNGSNRSHSASPMLAAAVAQGGYSAGNSLITSASSGSIGKWAASNORQINEQGGGESL 685 QY 626 HRNGSNRSSHSASPMLAAAVAQGGYSAGNSLITSASSGJGKWAASNORQINEQGGGESL 685 Db 1494 SLSDSTSTSNSGSASTSTSISNSASASESDSSSTSLSDSTSASNOSSESDSQSTSAS 1550 Qy 686 RNGNVSDCSSNNGGSSSLGYKKPSISVAKIIGGTDTSRFGASPNLLSQQHHSAHHLTHQQ 745 Db 1551 LSDSLGTSTSNR	1225 ESVSSSTSESTSLSDSTSESGSTSTSLSNSTSGSASISTSTSISESTSTFKS 334 EDLSRALQDVVANKLDARKGASQHHEQRSILDNRLFKMKHHDQEQDHDGDELED

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S-TSDSMSGSVSVSTSTS 1950
                               KCESEAATGHHSPGHHTT 1144
                                                            GGGGGGGGNGQTNGNGRSSRM 1087
| | : : | :
SSQSMSGSE-STSTSVSDSQS 1894
                                                                                                                           SESVSESTSLSDSIS----- 1836
                                                                                                                                                                                       SEGNGSAAGNGSNGSNGNGHG 975
                                                                                                                                                                                                                                                      SGSTSVSDSGSLSVSTSLRKS 1750
                                                                                                                                                                                                                                                                                   TNATNAYGLDFNRITEAMRNP 924
                                                                                                                                                                                                                                                                                                                                                                                   ----STSDSRSTSASTSTSMR 1632
                                                                                                                                                                                                                                                                                                                                                                                                                RGEMSVHRAGSYYGVPHSTLE 804
                                                                                                                                                                                                                                                                                                                                                                                                                                               GSTSESTSESDSTSTSLSDSQ 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASPNLLSQQHHSAHHLTHQQ 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKMMASNIQRQINEQSGQESL 685
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: | | | ::: | :::
ESDSQSISTSASESTSESAST 1493
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| : | : | | : | : | : | CONTROL |
QSTSTYTSQSTSQSESTSTST 1443
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                                                                                                                                                   -ESVKRSGSPMGNYADIKRER 1034
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963 GNGSNGSNGNGHGHGHGHGHALLDQLLVKKT	756	601 GGHHPLNNNNSLSISNNSHRNGSNRSP	389 NDDAEAEVDSNASTPVYPAEFARAQLRKLSHLSEHNGS-DLGEDVDRGSPKWGRHPAC-G
PLPFTNHRNNDYAAT 1008	GKYRNYDRDSLVEAVKAVORGEM	NNUNSLSISNNSNHSSNSHRNGSNRSP	INGS-DLGEDVDRGSPKWGRHPAC-G 446

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